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- ☐ 1. [20050227248](#). 08 Oct 04. 13 Oct 05. Polypeptides having beta-1,4-GalNAc transferase activity. Gilbert, Michel, et al. 435/6; 435/193 435/252.3 435/471 435/69.1 435/85 536/23.2 536/53 C12Q001/68 C07H021/04 C12P019/28 C12N009/10 C12N015/74 C12N001/21.
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- ☐ 2. [20050084891](#). 08 Oct 04. 21 Apr 05. Beta 1,4-N-acetylgalactosaminyl transferases from *C. jejuni*. Gilbert, Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 514/54 536/23.2 536/53 C12Q001/68 A61K031/739 C07H021/04 C08B037/00 C12N009/10 C12N015/74.
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- ☐ 3. [20050064550](#). 22 Apr 04. 24 Mar 05. Nucleic acids encoding beta 1,4-N-acetylgalactosaminyltransferases from *C. Jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/252.33 435/320.1 536/23.2 536/53 C12N009/10 C12N001/21 C12N015/74.
- 
- ☐ 4. [20050048630](#). 08 Oct 04. 03 Mar 05. Nucleic acids encoding beta 1,4-N-acetylgalactosaminyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/85; 435/193 435/252.3 435/320.1 435/69.1 514/54 536/23.2 536/53 C07H021/04 C08B037/00 A61K031/739 C12P019/28 C12N009/10 C12N015/74.
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- ☐ 5. [20040265875](#). 24 Apr 04. 30 Dec 04. Beta 1,4-N-acetylgalactosaminyltransferases form *C. jejuni*. Gilbert, Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 C12Q001/68 C07H021/04 C12N009/10 C08B037/00 C12N015/74.
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- ☐ 6. [20040259203](#). 19 May 04. 23 Dec 04. Nucleic acids encoding beta 1,3-galactosyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/252.3 435/320.1 514/54 536/23.2 536/53 C08B037/00 C07H021/04 C12N009/10.
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- ☐ 7. [20040259140](#). 21 May 04. 23 Dec 04. Beta 1,3-galactosyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 C12Q001/68 C07H021/04 C12P019/18 C08B037/00 C12N009/10.
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- ☐ 8. [20040229313](#). 08 Apr 04. 18 Nov 04. Sialyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/252.33 435/320.1 514/54 536/23.2 536/54 A61K031/739 C07H021/04 C12N009/10 C12N001/21 C12N015/74.
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- ☐ 9. [20040229272](#). 17 May 04. 18 Nov 04. Beta 1,3-galactosyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 435/89 536/23.2 536/53 C12Q001/68 C07H021/04 C12P019/30 C12N009/10 C12N015/74.
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- ☐ 10. [20040229263](#). 08 Apr 04. 18 Nov 04. Los locus from *C.jejuni*. Gilbert, Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 435/89 536/23.2 536/53 C12Q001/68 C07H021/04 C12P019/30 C12N009/10 C12N015/74.
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- ☐ 12. [20040203113](#). 12 May 04. 14 Oct 04. Nucleic acids encoding beta 1,4-N-

acetylgalactosaminyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/320.1 435/325 536/23.2 536/53 C12P019/18 C07H021/04 C12N009/10 C08B037/00.

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☐ 13. 20040203112. 12 May 04. 14 Oct 04. Beta1,4-N-acetylgalactosaminyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/320.1 435/325 536/23.2 536/53 C12P019/18 C07H021/04 C08B037/00 C12N009/10.

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☐ 14. 20040203103. 07 Apr 04. 14 Oct 04. Nucleic acids encoding sialyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/252.3 435/320.1 435/325 536/23.2 C12N009/10 C07H021/04 C12N001/21.

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☐ 15. 20040180406. 11 Dec 03. 16 Sep 04. Nucleic acids encoding sialyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/200 435/252.3 435/320.1 536/23.2 536/53 C12N009/10 C07H021/04 C08B037/00 C12N001/21 C12N015/74.

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☐ 16. 20040152165. 11 Mar 04. 05 Aug 04. Lipopolysaccharide alpha -2,3 sialyltransferase of *Campylobacter jejuni* and its uses. Gilbert, Michel, et al. 435/69.1; 435/193 435/320.1 435/325 536/23.2 536/53 C12N009/10 C07H021/04 C08B037/00.

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☐ 17. 20030186414. 11 Dec 02. 02 Oct 03. Nucleic acid that encodes a fusion protein. Gilbert, Michel, et al. 435/193; 435/320.1 435/325 435/6 435/69.1 536/23.2 C12N009/10 C12Q001/68 C07H021/04 C12P021/02 C12N005/06.

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☐ 19. 20030157658. 21 Nov 02. 21 Aug 03. Polypeptides having beta-1,4-GalNAc transferase activity. Gilbert, Michel, et al. 435/84; 435/193 435/252.33 435/320.1 435/69.1 536/23.2 536/53 C12P021/02 C12N001/21 C07H021/04 C08B037/00 C12P019/26 C12N009/10 C12N015/74.

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☐ 20. 20030157657. 21 Nov 02. 21 Aug 03. Polypeptides having beta-1,3-galactosyl transferase activity. Gilbert, Michel, et al. 435/84; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 C12P019/26 C07H021/04 C08B037/00 C12N009/10 C12P021/02 C12N001/21 C12N015/74.

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☐ 21. 20030157656. 21 Nov 02. 21 Aug 03. Nucleic acids encoding beta-1,4-GalNAc transferase. Gilbert, Michel, et al. 435/84; 435/193 435/252.33 435/320.1 435/69.1 536/23.2 536/53 C12P019/26 C08B037/00 C12N009/10 C07H021/04 C12P021/02 C12N001/21 C12N015/74.

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☐ 22. 20030157655. 21 Nov 02. 21 Aug 03. Nucleic acids encoding polypeptides with beta-1,3-galactosyl transferase activity. Gilbert, Michel, et al. 435/84; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 C12P019/26 C12P021/02 C12N001/21 C07H021/04 C08B037/00 C12N009/10 C12N015/74.

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☐ 23. 20030148459. 21 Nov 02. 07 Aug 03. Polypeptides having sialyltransferase activity. Gilbert, Michel, et al. 435/69.1; 435/193 435/252.3 435/320.1 536/23.2 536/53 C12P021/02 C12N001/21 C07H021/04 C12N009/10.

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C12N009/10 C12N015/74.

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- ☐ 25. [20020042369](#). 21 Mar 01. 11 Apr 02. Campylobacter glycosyltransferases for biosynthesis of gangliosides and ganglioside mimics. [Gilbert](#), Michel, et al. 514/12; 435/193 435/320.1 435/325 536/23.2 A61K038/17 C07H021/04 C12N009/10.
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- ☐ 26. [20020034805](#). 14 Dec 98. 21 Mar 02. FUSION PROTEINS FOR USE IN ENZYMATIC SYNTHESIS OF OLIGOSACCHARIDES. [GILBERT](#), MICHEL, et al. 435/193; 435/183 435/200 435/320.1 435/325 536/23.2 C12N009/00.
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- ☐ 27. [6911337](#). 21 Nov 02; 28 Jun 05. Nucleic acids encoding .beta.-1,4-GalNAc transferase. [Gilbert](#); Michel, et al. 435/252.3; 435/193 435/252.33 435/320.1 435/325 536/23.2. C07H021/04 C12N009/10 C12N015/00 C12N001/20.
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- ☐ 28. [6905867](#). 21 Nov 02; 14 Jun 05. Nucleic acids encoding polypeptides with .beta.1,3-galactosyl transferase activity. [Gilbert](#); Michel, et al. 435/252.3; 435/193 435/252.33 435/254.1 435/320.1 435/325 536/23.2. C12N009/10 C12N001/20 C12N015/00 C12N015/63 C07H021/04.
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- ☐ 30. [6723545](#). 21 Nov 02; 20 Apr 04. Polypeptides having .beta.-1,4-GalNAc transferase activity. [Gilbert](#); Michel, et al. 435/193;. C12N009/10.
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- ☐ 31. [6709834](#). 29 Jan 02; 23 Mar 04. Lipopolysaccharide .alpha.-2,3 sialyltransferase of campylobacter jejuni and its uses. [Gilbert](#); Michel, et al. 435/15; 435/183 435/193 435/220 435/252.3 435/320.1 435/4 435/41 435/6 435/7.2 435/85 435/97 530/350. C12Q001/48.
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- ☐ 32. [6699705](#). 21 Mar 01; 02 Mar 04. Campylobacter glycosyltransferases for biosynthesis of gangliosides and ganglioside mimics. [Gilbert](#); Michel, et al. 435/252.3; 435/193 435/252.33 435/320.1 435/325 536/23.2. C07H021/04 C12N001/20 C12N015/63 C12N009/10.
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- ☐ 33. [6689604](#). 18 Mar 99; 10 Feb 04. Lipopolysaccharide .alpha.-2,3 sialyltransferase of Campylobacter jejuni and its uses. [Gilbert](#); Michel, et al. 435/320.1; 435/252.3 435/252.33 435/346 435/6 435/68.1 435/69.1 435/69.3 435/70.2 435/71.1 435/71.2 435/74 435/822 514/54 536/23.1 536/23.2 536/24.3. C12N015/00.
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- ☐ 35. [6210933](#). 01 Sep 99; 03 Apr 01. Recombinant .alpha.-2,3-sialyltransferases and their uses. [Gilbert](#); Michel, et al. 435/97; 435/193 536/23.2. C12N009/10 C12N015/54 C12D019/18.
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- ☐ 36. [6096529](#). 07 Jun 97; 01 Aug 00. Recombinant .alpha.-2,3-sialyltransferases and their uses. [Gilbert](#); Michel, et al. 435/252.3; 435/193 435/252.33 435/320.1 435/325 536/23.2. C12N015/54 C12N001/21 C12N005/10 C12N009/10.
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- ☐ 37. [WO 200274942A](#). New glycosyltransferases from Campylobacter, useful for synthesizing gangliosides and ganglioside mimetics, and in studying the pathogenesis mechanisms of organisms that synthesize ganglioside mimetics. [GILBERT](#), M, et al. C07H021/04 C12N001/20 C12N005/10

C12N009/00 C12N009/10 C12N009/12 C12N015/09 C12N015/54 C12N015/63 C12Q001/68.

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☐ 39. WO 9949051A. New sialyltransferases useful for adding sialyl residues to acceptor molecules. GILBERT, M, et al. A61K039/02 C07H021/04 C08B037/00 C12N001/21 C12N005/10 C12N009/10 C12N015/00 C12N015/09 C12N015/54 C12N015/70 C12N015/74 C12N015/79 C12P019/26 C12P021/02 C12Q001/48 E21B034/10.

☐ 40. US 6096529A. Nucleic acid sequence encoding Neisseria alpha-2,3-sialyl:transferase - useful to add sialic acid to acceptor with terminal galactose residue for synthesis of biologically active oligosaccharide. GILBERT, M, et al. C12N001/15 C12N001/19 C12N001/21 C12N005/10 C12N009/10 C12N015/09 C12N015/54 C12N015/70 C12N015/79 C12P019/18 C12P019/26 C12N009/10 C12N015/09 C12R001:36 C12R001:36.

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## ENZYME: 2.4.99.-

Release 38, September 2005, and updates up to 06-Dec-2005

**Transferases**

**Glycosyltransferases**


**Transferring other glycosyl groups**

*All Swiss-Prot entries corresponding to class 2.4.99.-.*

The following ENZYME entries belong to class 2.4.99.-:

<a href="#">2.4.99.1</a>	Beta-galactoside alpha-2,6-sialyltransferase.
<a href="#">2.4.99.2</a>	Monosialoganglioside sialyltransferase.
<a href="#">2.4.99.3</a>	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase.
<a href="#">2.4.99.4</a>	Beta-galactoside alpha-2,3-sialyltransferase.
<a href="#">2.4.99.5</a>	Galactosyldiacylglycerol alpha-2,3-sialyltransferase.
<a href="#">2.4.99.6</a>	N-acetyllactosaminide alpha-2,3-sialyltransferase.
<a href="#">2.4.99.7</a>	(Alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl-galactosaminide 6-alpha-sialyltransferase.
<a href="#">2.4.99.8</a>	Alpha-N-acetylneuraminate alpha-2,8-sialyltransferase.
<a href="#">2.4.99.9</a>	Lactosylceramide alpha-2,3-sialyltransferase.
<a href="#">2.4.99.10</a>	Neolactotetraosylceramide alpha-2,3-sialyltransferase.
<a href="#">2.4.99.11</a>	Lactosylceramide alpha-2,6-N-sialyltransferase.

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## SEQUENCE LISTING

<110> Gilbert, Michel  
Wakarchuk, Warren W.  
National Research Council of Canada

<120> Lipopolysaccharide alpha-2,3 Sialyltransferase of  
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Phe Phe Pro Asp Ala Lys Leu Gly Tyr Glu Val Ile Glu Asn Leu Lys  
                                   115                                  120                                  125

Glu Phe Tyr Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr Phe Asn Lys Arg  
                                   130                                  135                                  140

Ile Thr Ser Gly Val Tyr Met Cys Ala Ile Ala Ile Ala Leu Gly Tyr  
                                   145                                  150                                  155                                  160

Lys Thr Ile Tyr Leu Cys Gly Ile Asp Phe Tyr Glu Gly Asp Val Ile  
 165 170 175  
 Tyr Pro Phe Glu Ala Met Ser Thr Asn Ile Lys Thr Ile Phe Pro Gly  
 180 185 190  
 Ile Lys Asp Phe Lys Pro Ser Asn Cys His Ser Lys Glu Tyr Asp Ile  
 195 200 205  
 Glu Ala Leu Lys Leu Leu Lys Ser Ile Tyr Lys Val Asn Ile Tyr Ala  
 210 215 220  
 Leu Cys Asp Asp Ser Ile Leu Ala Asn His Phe Pro Leu Ser Ile Asn  
 225 230 235 240  
 Ile Asn Asn Asn Phe Thr Leu Glu Asn Lys His Asn Asn Ser Ile Asn  
 245 250 255  
 Asp Ile Leu Leu Thr Asp Asn Thr Pro Gly Val Ser Phe Tyr Lys Asn  
 260 265 270  
 Gln Leu Lys Ala Asp Asn Lys Ile Met Leu Asn Phe Tyr Asn Ile Leu  
 275 280 285  
 His Ser Lys Asp Asn Leu Ile Lys Phe Leu Asn Lys Glu Ile Ala Val  
 290 295 300  
 Leu Lys Lys Gln Thr Thr Gln Arg Ala Lys Ala Arg Ile Gln Asn His  
 305 310 315 320  
 Leu Ser Tyr Lys Leu Gly Gln Ala Leu Ile Ile Asn Ser Lys Ser Val  
 325 330 335  
 Leu Gly Phe Leu Ser Leu Pro Phe Ile Ile Leu Ser Ile Val Ile Ser  
 340 345 350  
 His Lys Gln Glu Gln Lys Ala Tyr Lys Phe Lys Val Lys Lys Asn Pro  
 355 360 365  
 Asn Leu Ala Leu Pro Pro Leu Glu Thr Tyr Pro Asp Tyr Asn Glu Ala  
 370 375 380  
 Leu Lys Glu Lys Glu Cys Phe Thr Tyr Lys Leu Gly Glu Glu Phe Ile  
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 Lys Ala Gly Lys Asn Trp Tyr Gly Glu Gly Tyr Ile Lys Phe Ile Phe  
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 Lys Asp Val Pro Arg Leu Lys Arg Glu Phe Glu Lys Gly Glu  
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<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CJ18F 5' primer

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<212> DNA  
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<210> 5  
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<220>  
<223> Haemophilus influenzae Rd putative open reading  
frame (ORF)

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1 5 10 15  
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20 25 30  
Val Gln Lys Leu Leu Thr Gln Val Asp Ile Gly His Tyr Tyr Leu Asn  
35 40 45  
Lys Leu Pro Ala Phe Asp Ala Tyr Leu Gln Tyr Asn Glu Leu Tyr Glu  
50 55 60  
Asn Lys Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Thr Val  
65 70 75 80  
Met Gly Tyr Lys Asp Leu Tyr Leu Thr Gly Ile Asp Phe Tyr Gln Glu  
85 90 95  
Lys Gly Asn Pro Tyr Ala Phe His His Gln Lys Glu Asn Ile Ile Lys  
100 105 110  
Leu Leu Pro Ser Phe Ser Gln Asn Lys Ser Gln Ser Asp Ile His Ser  
115 120 125  
Met Glu Tyr Asp Leu Asn Ala Leu Tyr Phe Leu Gln Lys His Tyr Gly  
130 135 140  
Val Asn Ile Tyr Cys Ile Ser Pro Glu Ser Pro Leu Cys Asn Tyr Phe  
145 150 155 160  
Pro Leu Ser Pro Leu Asn Asn Pro Ile Thr Phe Ile Leu Glu Glu Lys  
165 170 175  
Lys Asn Tyr Thr Gln Asp Ile Leu Ile Pro Pro Lys Phe Val Tyr Lys  
180 185 190

Lys Ile Gly Ile Tyr Ser Lys Pro Arg Ile Tyr Gln Asn Leu Ile Phe  
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 (His)6

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<220>  
 <223> Description of Artificial Sequence:linker between  
 two fusion protein domains

<400> 7  
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# Search in UniProt Knowledgebase (Swiss-Prot and TrEMBL) for: campylobacter sialyltransferase

**UniProtKB/Swiss-Prot Release 48.6 of 06-Dec-2005**  
**UniProtKB/TrEMBL Release 31.6 of 06-Dec-2005**

- 
- Number of sequences found in UniProt Knowledgebase (Swiss-Prot<sub>(0)</sub> and TrEMBL) (15): **15**
  - Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
  - For more directed searches, you can use the Sequence Retrieval System SRS.
- 

***Search in UniProtKB/Swiss-Prot: There are matches to 0 out of 201594 entries***

---

***Search in UniProtKB/TrEMBL: There are matches to 15 out of 2484574 entries***

Q32VR8\_CAMJE

Alpha-2,3-sialyltransferase {GENE:Name=cstI} - Campylobacter jejuni subsp. jejuni

Q4HEJ9\_CAMCO

Alpha-2,3-sialyltransferase {GENE:ORFNames=CCO1538} - Campylobacter coli RM2228

Q4HEK5\_CAMCO

Alpha-2,3-sialyltransferase {GENE:ORFNames=CCO1544} - Campylobacter coli RM2228

Q4HEL4\_CAMCO

Alpha-2,3-sialyltransferase {GENE:ORFNames=CCO1527} - Campylobacter coli RM2228

Q4HGT1\_CAMCO

Bifunctional alpha-2,3/-2,8-sialyltransferase {GENE:ORFNames=CCO1215} - Campylobacter coli RM2228

Q5DT12\_CAMJE

Putative alpha-2,3/-2,8 sialyltransferase - Campylobacter jejuni  
Q7BP25\_CAMJE  
Hypothetical protein Cj1140 (2,3-sialyl transferase) (Alpha-2,3-sialyltransferase)  
{GENE:Name=cstIII; Synonyms=cst-III; OrderedLocusNames=Cj1140} -  
Campylobacter jejuni  
Q938X6\_CAMJE  
Alpha-2,3-/alpha-2,8-sialyltransferase {GENE:Name=cstII} - Campylobacter jejuni  
Q93CZ5\_CAMJE  
Bifunctional alpha-2,3/-2,8-sialyltransferase {GENE:Name=cst-II} - Campylobacter  
jejuni  
Q93D05\_CAMJE  
Alpha-2,3-sialyltransferase {GENE:Name=cst-II} - Campylobacter jejuni  
Q93MQ0\_CAMJE  
Alpha-2,3-/alpha-2,8-sialyltransferase {GENE:Name=cstII} - Campylobacter jejuni  
Q9F0M9\_CAMJE  
Alpha-2,3-sialyltransferase {GENE:Name=cst-II} - Campylobacter jejuni  
Q9L9Q5\_CAMJE  
Alpha-2,3-sialyltransferase {GENE:Name=cst-II; Synonyms=cst, cstII} -  
Campylobacter jejuni  
Q9LAK3\_CAMJE  
Alpha-2,3/8-sialyltransferase (Alpha-2,3/-2,8-sialyltransferase) {GENE:Name=cst-II}  
- Campylobacter jejuni  
Q9RGF1\_CAMJE  
Alpha-2,3-sialyltransferase {GENE:Name=cst-I} - Campylobacter jejuni

---

in Swiss-Prot/TrEMBL by AC, ID, description,  
gene name, organism  
**Please do NOT use any boolean operators  
(and, or, etc.)**

---

If you would like to retrieve all the Swiss-Prot/TrEMBL entries contained in this list, you  
can enter a file name. These entries will then be saved to a file under this name in the  
directory outgoing of the ExpASY anonymous ftp server, from where you can download  
it. (Please note that this temporary file will only be kept for 1 week.)

File name:

Format: ☒ Swiss-Prot ☐ Fasta

or



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If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:  
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query: 22 AA

Date run: 2005-12-15 23:01:28 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

2,699,091 sequences; 880,353,591 total letters

UniProt Knowledgebase Release 6.6 consists of:

UniProtKB/Swiss-Prot Release 48.6 of 06-Dec-2005: 201594 entries

UniProtKB/TrEMBL Release 31.6 of 06-Dec-2005: 2484574 entries

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Db	AC	Description
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<input type="checkbox"/>	sp P72074	LST_NEIGO CMP-N-acetylneuraminate-beta-galactosamide-a.
--------------------------	-----------	---

<input type="checkbox"/>	tr Q5F7T9	_NEIG1 Alpha-2,3-sialyltransferase [NGO1081] [Neisseria
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CLUSTAL FORMAT for T-COFFEE Version 1.37, CPU=0.00 sec, SCORE=6070, Nseq=2, Len=431

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                                     *.....*:.*..*..*.:*****
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unk|VIRT7553|Blast_submission KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNF  
tr|Q93MQ0|Q93MQ0_CAMJE      KAVFYNPGLFFEQYYTLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDY  
*****:*.....* *... :*** :*.**.* ..*:..*:..*
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tr|Q93MQ0|Q93MQ0_CAMJE           YDFFKQLKEFNAYFKFHEIYLNQRITSGVYMCAVAIALGYKEIYLSGIDFYQN
*.:.:***** **.:.:*****.:*****.:***** *** *****:
```

```
unk|VIRT7553|Blast_submission AMSTNIKTIFPGIKDFKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSLA
tr|Q93MQ0|Q93MQ0_CAMJE TKQENLLKLAPDFKNDRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLA
: . *: : *::: : ***: **::*: : **:~* ** :***
```

```
unk|VIRT7553|Blast_submission      NINNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSKD
tr|Q93MQ0|Q93MQ0_CAMJE              NLNSNFI IQEK-NNYTKDILIPSS EAYGKF SKN-----INF-----
*. ** * : . : * **   : * * : * * *          * **           . **
```

```
unk|VIRT7553|Blast_submission    KEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVIS
tr|Q93MQ0|Q93MQ0_CAMJE          -----
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unk|VIRT7553|Blast_submission      YKFKVKKNPNLALPPLETYPDYNEALKEKECFYKLGEEFIKAGKNWYGEgyI
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                                     : * ** : *** : : : :
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tr|Q93MQ0|Q93MQ0_CAMJE              PSDIKHYFKGK
*      .      .      .      .      .
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CLUSTAL FORMAT for T-COFFEE Version\_1.37, CPU=0.00 sec, SCORE=6070, Nseq=2, Len=431

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unk|VIRT7553|Blast_submission  MTRTRMENELIVSKNMQNI IAGNGPSLKNIN YKRLPREYDVFR CNQFYFEDK
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                               *::: ** :*****: *: *.***.::: *****
unk|VIRT7553|Blast_submission  KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNL PFIESNDFLHQFYNF
tr|Q93MQ0|Q93MQ0_CAMJE      KAVFYNPGLFFEQYYTLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDY
                               ****:***: *::: ** * :*** : *: **.:* ..*:..*:::: **::
unk|VIRT7553|Blast_submission  YEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEG
tr|Q93MQ0|Q93MQ0_CAMJE      YDFFKQLKEFNAYFKFHEIYLNQRITSGVYMCAVAIALGYKEIYLSGIDFYQN
                               *:..*:*** **:*::***:*.*****:***** ***.*****:..
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tr|Q93MQ0|Q93MQ0_CAMJE      TKQENLLKLAPDFKNDRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLA
                               : . *: .: *.:*: :.      ***: **:*:::*. **:::*.** *:**
unk|VIRT7553|Blast_submission  NINNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNI LHSKD
tr|Q93MQ0|Q93MQ0_CAMJE      NLNSNFIIQEK-NNYTKDILIPSEAYGKFSKN-----INF-----
                               *:*.** :::* ** :***:..* . . * **      :**
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tr|Q93MQ0|Q93MQ0_CAMJE      -----KKIKIKENIYYKLIDLLR-----
                               : :* ** : *** ::::
unk|VIRT7553|Blast_submission  PRLKREFEKGE
tr|Q93MQ0|Q93MQ0_CAMJE      PSDIKHYFKGK
                               *   :.: **;

```

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If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:  
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Query: 430 AA

Date run: 2005-12-15 16:31:23 UTC+0100 on sib-gm1.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

2,699,091 sequences; 880,353,591 total letters

UniProt Knowledgebase Release 6.6 consists of:

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UniProtKB/TrEMBL Release 31.6 of 06-Dec-2005: 2484574 entries

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Db	AC	Description
----	----	-------------



- |                          |           |  |
|--------------------------|-----------|--|
| <input type="checkbox"/> | tr Q32VR8 | _CAMJE Alpha-2,3-sialyltransferase [cstI] [Campylobacter]  |
| <input type="checkbox"/> | tr Q9RGF1 | _CAMJE Alpha-2,3-sialyltransferase [cst-I] [Campylobacter] |

☐ tr Q5DT12 \_CAMJE Putative alpha-2,3/-2,8 sialyltransferase [Campy  
☐ tr Q93MQ0 \_CAMJE Alpha-2,3-/alpha-2,8-sialyltransferase [cstII] [  
☐ tr Q9F0M9 \_CAMJE Alpha-2,3-sialyltransferase [cst-II] [Campylobac  
☐ tr Q9LAK3 \_CAMJE Alpha-2,3/8-sialyltransferase (Alpha-2,3-/2,8-si  
☐ tr Q9L9Q5 \_CAMJE Alpha-2,3-sialyltransferase [cst-II] [Campylobac  
☐ tr Q938X6 \_CAMJE Alpha-2,3-/alpha-2,8-sialyltransferase [cstII] [  
☐ tr Q50FZ0 \_CAMJE Cj81-011 (Fragment) [Campylobacter jejuni]  
☐ tr Q93CZ5 \_CAMJE Bifunctional alpha-2,3/-2,8-sialyltransferase [c  
☐ tr Q93D05 \_CAMJE Alpha-2,3-sialyltransferase [cst-II] [Campylobac  
☐ tr Q7BP25 \_CAMJE Hypothetical protein Cj1140 (2,3-sialyl transfer  
☐ tr Q32VQ2 \_CAMJE Putative glycosyltransferase [Campylobacter jeju  
☐ tr Q4QM36 \_HAEI8 CMP-neu5Ac--lipooligosaccharide alpha 2-3 sialyl  
☐ tr Q32VR2 \_CAMJE Putative glycosyltransferase [Campylobacter jeju  
☐ tr Q5W602 \_CAMJE Putative glycosyltransferase [Campylobacter jeju  
☐ tr Q5M6Q2 \_CAMJE Putative sugar transferase [HS23.17] [Campylobac  
☐ tr Q9CLP3 \_PASMU Hypothetical protein PM1174 [PM1174] [Pasteurell  
☐ tr Q6EF79 \_CAMJE Putative glycosyltransferase [Campylobacter jeju  
☐ tr Q4QNI8 \_HAEI8 CMP-Neu5Ac--lipooligosaccharide alpha 2-3 sialyl  
☐ tr Q6EF56 \_CAMJE Putative glycosyltransferase [Campylobacter jeju  
☐ tr Q5W603 \_CAMJE Hypothetical protein [Campylobacter jejuni]  
☐ tr Q32VQ8 \_CAMJE Hypothetical protein [Campylobacter jejuni subsp  
☐ tr Q32VR3 \_CAMJE Hypothetical protein [Campylobacter jejuni subsp  
☐ tr Q32VQ3 \_CAMJE Hypothetical protein [Campylobacter jejuni subsp  
☐ tr Q5HT01 \_CAMJR Capsular polysaccharide biosynthesis protein, pu  
☐ tr Q5M6U5 \_CAMJE Putative sugar transferase [HS41.06] [Campylobac  
☐ tr Q6EBB5 \_CAMJE Tgh007 (Fragment) [Campylobacter jejuni]  
☐ tr Q4HEK5 \_CAMCO Alpha-2,3-sialyltransferase [CC01544] [Campyloba  
☐ tr Q4HEL4 \_CAMCO Alpha-2,3-sialyltransferase [CC01527] [Campyloba  
☐ tr Q4HEJ9 \_CAMCO Alpha-2,3-sialyltransferase [CC01538] [Campyloba  
☐ sp P24324 Y352\_HAEIN Hypothetical protein HI0352 (ORF1) [HI0352].  
☐ tr Q5M6M2 \_CAMJE Putative sugar transferase [HS19.11] [Campylobac  
☐ tr Q5M6M5 \_CAMJE Putative sugar transferase [HS19.08] [Campylobac  
☐ tr Q5HT02 \_CAMJR Capsular polysaccharide biosynthesis protein, pu  
☐ tr Q4HR89 \_CAMUP Hypothetical protein [CUP1274] [Campylobacter up  
☐ tr Q4HEL1 \_CAMCO DcbE, putative [CC01537] [Campylobacter coli RM2  
☐ tr Q9PMM6 \_CAMJE Hypothetical protein Cj1431c [Cj1431c] [Campylob  
☐ tr Q50FV9 \_CAMJE Cj81-063 (Fragment) [Campylobacter jejuni]  
☐ tr Q4HR98 \_CAMUP Hypothetical protein [CUP1265] [Campylobacter up  
☐ tr Q4HKU2 \_CAMLA Glycosyl transferase family 8 family [CLA1010] [  
☐ tr Q5M6U6 \_CAMJE Putative sugar transferase [HS41.05] [Campylobac  
☐ tr Q5M6S8 \_CAMJE Putative sugar transferase [HS41.23] [Campylobac  
☐ tr Q6EF57 \_CAMJE Putative glycosyltransferase (Putative sugar tra

☐ tr Q4HR96 \_CAMUP Glycosyl transferase, group 2 family protein [CU  
☐ tr Q4HLH9 \_CAMLA Hypothetical protein [CLA0678] [Campylobacter la  
☐ tr Q9PMN6 \_CAMJE Possible sugar transferase [Cj1421c] [Campylobac  
☐ tr Q9PMN5 \_CAMJE Possible sugar transferase [Cj1422c] [Campylobac  
☐ tr Q6EF89 \_CAMJE Putative glycosyltransferase [Campylobacter jeju  
☐ tr Q6EF76 \_CAMJE Putative glycosyltransferase [Campylobacter jeju  
☐ tr Q5M6M6 \_CAMJE Putative sugar transferase [HS19.07] [Campylobac  
☐ tr Q9PMM3 \_CAMJE Putative sugar transferase [Cj1434c] [Campylobac  
☐ tr Q4HR95 \_CAMUP Glycosyl transferase, group 2 family protein, pu  
☐ tr Q5M6R2 \_CAMJE Putative sugar transferase [HS23.07] [Campylobac  
☐ tr Q5M6P9 \_CAMJE Putative sugar transferase (Cj81-080) [HS23.20]  
☐ tr Q4HRA0 \_CAMUP Glycosyl transferase family 8 family [CUP1263] [  
☐ tr Q4HSD1 \_CAMUP Probable sugar transferase Cj1422c [CUP0322] [Ca  
☐ tr Q4HQ44 \_CAMUP Probable sugar transferase Cj1422c [CUP1233] [Ca  
☐ tr Q4HLH0 \_CAMLA Probable sugar transferase Cj1422c [CLA0667] [Ca  
☐ tr Q4HLF9 \_CAMLA Probable sugar transferase Cj1421c [CLA0655] [Ca  
☐ tr Q4HNW9 \_CAMUP Capsular polysaccharide biosynthesis protein, pu  
☐ tr Q9PML9 \_CAMJE Putative sugar transferase [Cj1438c] [Campylobac  
☐ tr Q4HQ73 \_CAMUP Capsular polysaccharide biosynthesis protein, pu  
☐ tr Q9PMM5 \_CAMJE Putative sugar transferase [Cj1432c] [Campylobac  
☐ tr Q4HTL3 \_CAMUP Hypothetical protein [CUP0667] [Campylobacter up  
☐ tr Q5M6N9 \_CAMJE Putative sugar transferase [HS1.07] [Campylobact  
☐ tr Q50FW8 \_CAMJE Cj81-047 (Fragment) [Campylobacter jejuni]  
☐ tr Q5M6S9 \_CAMJE Putative sugar transferase [HS41.22] [Campylobac  
☐ tr Q9CMP1 \_PASMU HyaE (FcbE) [hyaE] [Pasteurella multocida]  
☐ tr Q4HGT1 \_CAMCO Bifunctional alpha-2,3/-2,8-sialyltransferase [C  
☐ tr O85456 \_PASMU HyaE [hyaE] [Pasteurella multocida]  
☐ tr Q4HS04 \_CAMUP Hypothetical protein [CUP1761] [Campylobacter up  
☐ tr Q9AHN3 \_PASMU DcbE [dcbE] [Pasteurella multocida]  
☐ tr Q8L0V3 \_ECOLI Hypothetical protein kfoB [kfoB] [Escherichia co.  
☐ tr Q6EBB2 \_CAMJE Tgh012 (Fragment) [Campylobacter jejuni]  
☐ tr Q4HTC3 \_CAMUP Capsular polysaccharide biosynthesis protein, pu  
☐ tr Q6KCZ4 \_ECOLI KfiB protein [kfiB] [Escherichia coli]  
☐ tr Q43KB3 \_9CHLB Similar to Chromosome segregation ATPases [Cpha2  
☐ tr Q6EBB6 \_CAMJE Tgh006 (Fragment) [Campylobacter jejuni]  
☐ tr Q6EB08 \_CAMJE Tgh120 (Fragment) [Campylobacter jejuni]  
☐ tr Q8IBW2 \_PLAF7 Hypothetical protein MAL7P1.65 [MAL7P1.65] [Plas  
☐ tr Q4Y918 \_PLACH Hypothetical protein (Fragment) [PC000047.00.0]  
☐ tr Q4HTQ9 \_CAMUP Hypothetical protein [CUP0614] [Campylobacter up  
☐ tr Q9EMR1 \_AMEPV AMV138 [AMV138] [Amsacta moorei entomopoxvirus (  
☐ tr Q7RS84 \_PLAYO TERT (Fragment) [PY00479] [Plasmodium yoelii yoe  
☐ tr Q8I474 \_PLAF7 Hypothetical protein PFE0130c [PFE0130c] [Plasmo

- ☐ tr Q8I3Z1 \_PLAF7 Hypothetical protein PFE0570w [PFE0570w] [Plasmo
- ☐ tr Q55FU8 \_DICDI Hypothetical protein [DDB0189664] [Dictyostelium
- ☐ tr Q7RCB6 \_PLAYO Hypothetical protein [PY05868] [Plasmodium yoeli
- ☐ tr Q8ILS2 \_PLAF7 Hypothetical protein [PF14\_0172] [Plasmodium fal
- ☐ tr Q4YMV9 \_PLABE Hypothetical protein (Fragment) [PB001093.03.0]
- ☐ tr Q6EF78 \_CAMJE Putative glycosyltransferase (Putative sugar tra
- ☐ tr Q6EF55 \_CAMJE Putative glycosyltransferase [Campylobacter jeju
- ☐ tr Q98RL8 \_GUITH Hypothetical protein orf714 [orf714] [Guillardia
- ☐ tr Q7QPQ2 \_GIALA GLP\_348\_13351\_18885 [Giardia lamblia ATCC 50803]
- ☐ tr P73984 \_SYNY3 Slr2117 protein [slr2117] [Synechocystis sp. (st
- ☐ tr Q5M6S3 \_CAMJE Putative sugar transferase [HS41.28] [Campylobac
- ☐ tr Q8EWI3 \_MYCPE Hypothetical protein MYPE2220 [MYPE2220] [Mycopl
- ☐ tr Q8I232 \_PLAF7 Hypothetical protein PFA0550w [PFA0550w] [Plasmo
- ☐ tr Q8IDZ6 \_PLAF7 Hypothetical protein PF13\_0182 [PF13\_0182] [Plas

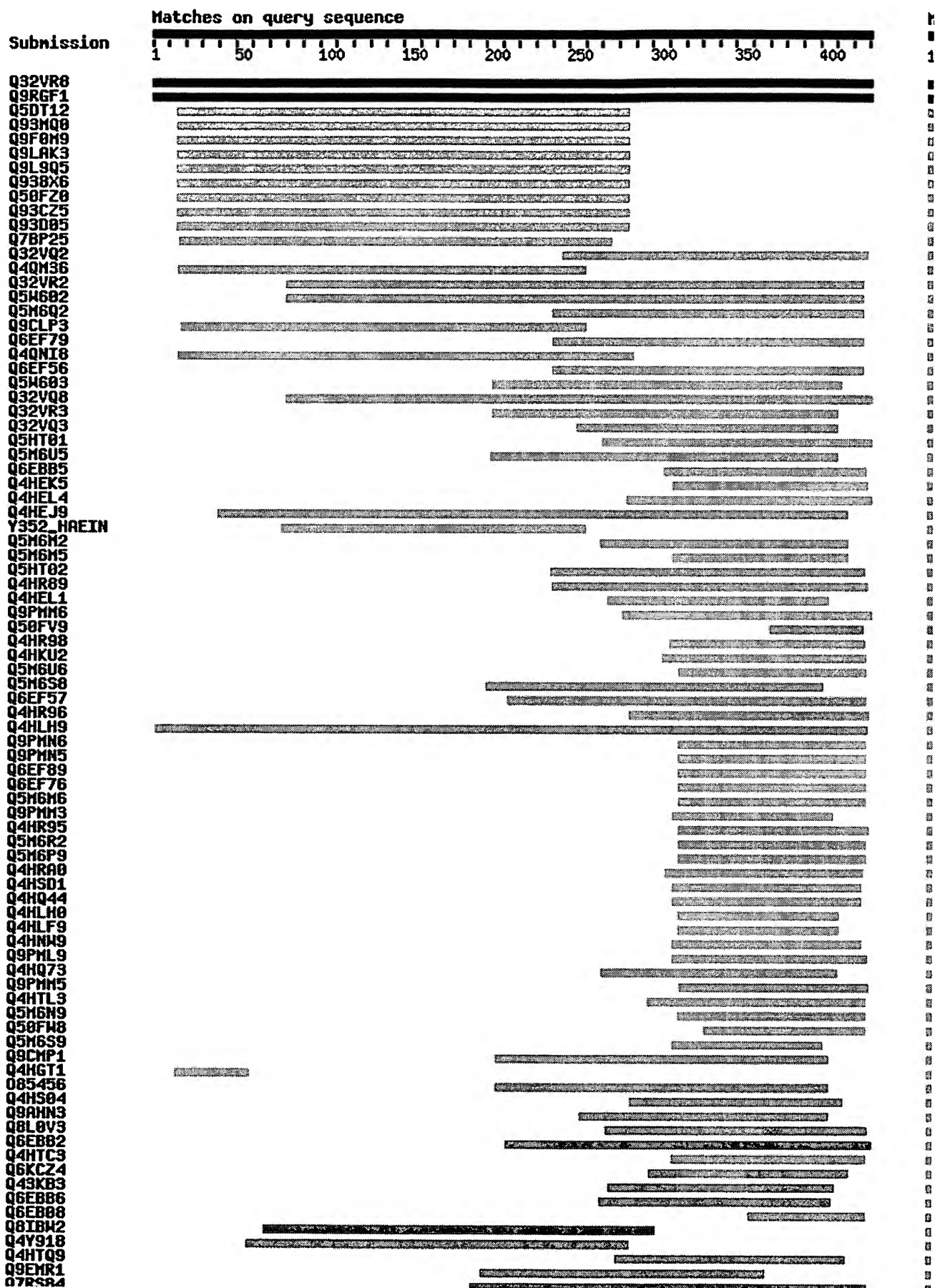
### Graphical overview of the alignments

 to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs  
( Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits

CST-I



**Alignments**

tr Q32VR8 Alpha-2,3-sialyltransferase [cstI] [Campylobacter  
Q32VR8\_CAMJE jejuni subsp.  
jejuni]

Score = 877 bits (2266), Expect = 0.0  
Identities = 430/430 (100%), Positives = 430/430 (100%)

Query: 1 MTRTRMENELIVSKNMQNIIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKYYL  
MTRTRMENELIVSKNMQNIIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKYYL  
Sbjct: 1 MTRTRMENELIVSKNMQNIIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKYYL

Query: 61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLFPFIESNDFLHQFYNFFPD  
KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLFPFIESNDFLHQFYNFFPD  
Sbjct: 61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLFPFIESNDFLHQFYNFFPD

Query: 121 YEVIENTLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI  
YEVIENTLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI  
Sbjct: 121 YEVIENTLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI

Query: 181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDASILANHFP  
AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDASILANHFP  
Sbjct: 181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDASILANHFP

Query: 241 INNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSDKDTLIK  
INNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSDKDTLIK  
Sbjct: 241 INNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSDKDTLIK

Query: 301 EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQE  
EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQE  
Sbjct: 301 EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQE

Query: 361 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIF  
KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIF  
Sbjct: 361 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIF

Query: 421 RLKREFEKGE 430  
RLKREFEKGE  
Sbjct: 421 RLKREFEKGE 430

tr Q9RGF1 Alpha-2,3-sialyltransferase [cst-I] [Campylobacter  
Q9RGF1\_CAMJE jejuni]

Score = 875 bits (2261), Expect = 0.0

Identities = 429/430 (99%), Positives = 429/430 (99%)

```

Query: 1  MTRTRMENELIVSKNMQNI IIIAGNGPSLKNINYKRLPREYDVFR CNQFYFEDKYYL
          MTRTRMENELIVSKNMQNI IIIAGNGPSLKNINYKRLPREYDVFR CNQFYFEDKYYL
Sbjct: 1  MTRTRMENELIVSKNMQNI IIIAGNGPSLKNINYKRLPREYDVFR CNQFYFEDKYYL

Query: 61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFY NFFPD
          KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFY NFFPD
Sbjct: 61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFY NFFPD

Query: 121 YEV IENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI
          YEV IENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI
Sbjct: 121 YEV IENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI

Query: 181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDD SILANHFP
          AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDD SILANHFP
Sbjct: 181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDD SILANHFP

Query: 241 INN NFTLENKHNN SINDILLTDNTPGV SFYKNQLKADNKIMLNFY NILH SKDTLIK
          INN NFTLENKHNN SINDILLTDNTPGV SFYKNQLKADNKIMLNFY NILH SKD LIK
Sbjct: 241 INN NFTLENKHNN SINDILLTDNTPGV SFYKNQLKADNKIMLNFY NILH SKDNLIK

Query: 301 EIAVLKKQTTQRAKARIQNHL SYKLGQALIINSKSVLGFLSLPFIILSIVISHKQE
          EIAVLKKQTTQRAKARIQNHL SYKLGQALIINSKSVLGFLSLPFIILSIVISHKQE
Sbjct: 301 EIAVLKKQTTQRAKARIQNHL SYKLGQALIINSKSVLGFLSLPFIILSIVISHKQE

Query: 361 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGE GYIKFIF
          KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGE GYIKFIF
Sbjct: 361 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGE GYIKFIF

Query: 421 RLKREFEKGE 430
          RLKREFEKGE
Sbjct: 421 RLKREFEKGE 430

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tr  Q5DT12          Putative alpha-2,3/-2,8 sialyltransferase
    Q5DT12_CAMJE    [Campylobacter jejuni]

```

Score = 301 bits (770), Expect = 3e-80

Identities = 147/274 (53%), Positives = 189/274 (68%), Gaps = 7/27

```

Query: 16  MQNI IIIAGNGPSLKNINYKRLPREYDVFR CNQFYFEDKYYLGKKIKAVFFNPGVFL
          M+ +IIAGNGPSLK I+Y RLP ++DVFR CNQFYFEDKYYLGKK KAVF+NP +F
Sbjct: 1  MKKVIIAGNGPSLKEIDYSRLPNDFDVFR CNQFYFEDKYYLGKKCKAVFY NPSLFF

Query: 76  TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFY NFFPD AKLGYEVIENLKEFY

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      T K LI   EYE + I CS FNL   IES +FL  FY++FPDA LGY+   + LKEF
Sbjct: 61  TLKHLIQNQEYETELIVCSNFNLTTHIESENFLKNFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
      ++EIYFN+RITSG+YMCA+AIALGYK IYL GIDFY+   Y F+   N+   +
Sbjct: 121 FHEIYFNQRITSGIYMCAVAIALGYKEIYLSGIDFYQNGSSYAFDTKQKNLLKL--

Query: 196 FKPSNC----HSKEYDIEALKLLKSIYKVNIYALCDDASILANHFPLSININNNFTL
      FK N      HSK  D++AL+ L+  YK+ +Y LC +S+LAN  L+ N+N+NF +
Sbjct: 178 FKNDNSHYIGHSKNTDLKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFII

Query: 252 NNSINDILLTDNTPGVSFYKNQLKADNKIMLNFY 285
      NN  DIL+  +      F KN +      KI  N Y
Sbjct: 238 NNYTKDILIPSSEAYGKFSKNIIFKKIKIKENIY 271

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tr   Q93MQ0                Alpha-2,3-/alpha-2,8-sialyltransferase [cstII]
      Q93MQ0_CAMJE          [Campylobacter
                          jejuni]

```

Score = 290 bits (742), Expect = 6e-77

Identities = 142/271 (52%), Positives = 186/271 (68%), Gaps = 2/27

```

Query: 16  MQNIIIIAGNGPSLKNINIKRLPREYDVFRCNQFYFEDKYYLGKKIKAVFFNPGVFL
      M+ +II+GNGPSLK I+Y RLP ++DVFRCNQFYFEDKYYLGKK KAVF+NPG+F
Sbjct: 1   MKKVIIISGNGPSLKEIDYSRLPNDFDVFRCNQFYFEDKYYLGKKFKAVFYNPGLFF

Query: 76  TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENTLKEFY
      T K LI   EYE + I CS +N   +E+ +F+  FY++FPDA LGY+   + LKEF
Sbjct: 61  TLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
      ++EIY N+RITSGVYMCA+AIALGYK IYL GIDFY+   Y F+   N+   + P
Sbjct: 121 FHEIYLNQRITSGVYMCAVAIALGYKEIYLSGIDFYQNGSSYAFDTKQENLLKLAP

Query: 196 FKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDASILANHFPLSININNNFTLENK
      +      HSK  DI+AL+ L+  YK+ +Y LC +S+LAN  L+ N+N+NF ++ K
Sbjct: 181 DRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285
      DIL+  +      F KN      KI  N Y
Sbjct: 240 TKDILIPSSEAYGKFSKNINFKKIKIKENIY 270

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tr   Q9F0M9                Alpha-2,3-sialyltransferase [cst-II] [Campylobacter

```

Q9F0M9\_CAMJE                    jejuni]

Score = 290 bits (741), Expect = 8e-77

Identities = 143/271 (52%), Positives = 185/271 (67%), Gaps = 2/27

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRNCQFYFEDKYYLGKKIKAVFFNPGVFL  
M+ +IIAGNGPSLK I+Y RLP ++DVFRNCQFYFEDKYYLGKK KAVF+ PG F  
Sbjct: 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFRNCQFYFEDKYYLGKKCKAVFYTPGFFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDACLGYEVIENLKEFY  
T K LI EYE + I CS +N +E+ +F+ FY++FPDA LGY+ + LKEF  
Sbjct: 61 TLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP  
++EIYFN+RITSGVYMCA+AIALGYK IYL GIDFY+ Y F+ N+ + P  
Sbjct: 121 FHEIYFNQRITSGVYMCAVAIALGYKEIYLSGIDFYQNGSSYAFDTKQENLLKLAP

Query: 196 FKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK  
+ HSK DI+AL+ L+ YK+ +Y LC +S+LAN L+ N+N+NF ++ K  
Sbjct: 181 DRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285  
DIL+ + F KN KI N Y  
Sbjct: 240 TKDILIPSSEAYGKFSKNINFKKIKIKENVY 270

tr Q9LAK3                    Alpha-2,3/8-sialyltransferase (Alpha-2,3-/2,8-  
Q9LAK3\_CAMJE                    sialyltransferase)  
                              [cst-II] [Campylobacter jejuni]

Score = 288 bits (736), Expect = 3e-76

Identities = 143/271 (52%), Positives = 185/271 (67%), Gaps = 2/27

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRNCQFYFEDKYYLGKKIKAVFFNPGVFL  
M+ +IIAGNGPSLK I+Y RLP ++DVFRNCQFYFEDKYYLGKK KAVF+NP +F  
Sbjct: 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFRNCQFYFEDKYYLGKKCKAVFYNPILFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDACLGYEVIENLKEFY  
T K LI EYE + I CS +N +E+ +F+ FY++FPDA LGY+ + LK+F  
Sbjct: 61 TLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDYFPDAHLGYDFFKQLKDFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP  
++EIYFN+RITSGVYMCA+AIALGYK IYL GIDFY+ Y F+ N+ + P  
Sbjct: 121 FHEIYFNQRITSGVYMCAVAIALGYKEIYLSGIDFYQNGSSYAFDTKQKNLLKLAP

Query: 195 DFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK  
D HSK DI+AL+ L+ YK+ +Y LC +S+LAN L+ N+N+NF ++ K

Sbjct: 181 DNSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285

DIL+ + F KN KI N Y

Sbjct: 240 TKDILIPSSEAYGKFSKNINFKKIKIKENIY 270

tr Q9L9Q5 Alpha-2,3-sialyltransferase [cst-II] [Campylobacter  
Q9L9Q5\_CAMJE jejuni]

Score = 287 bits (735), Expect = 4e-76

Identities = 142/271 (52%), Positives = 184/271 (67%), Gaps = 2/27

Query: 16 MQNIIIIAGNGPSLKNINYKRLPREYDVFRNCQFYFEDKYYLGKKIKAVFFNPGVFL  
M+ +IIAGNGPSLK I+Y RLP ++DVFRNCQFYFEDKYYLGKK KAVF+ P F

Sbjct: 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFRNCQFYFEDKYYLGKKCKAVFYTPNFFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENTLKEFY  
T K LI EYE + I CS +N +E+ +F+ FY++FPDA LGY+ + LKEF

Sbjct: 61 TLKHLIQNQEYETELIMCSNYNQAHLNENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP  
++EIYFN+RITSGVYMCA+AIALGYK IYL GIDFY+ Y F+ N+ + P

Sbjct: 121 FHEIYFNQRITSGVYMCAVAIAIALGYKEIYLSGIDFYQNGSSYAFDTKQENLLKLAP

Query: 196 FKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK  
+ HSK DI+AL+ L+ YK+ +Y LC +S+LAN L+ N+N+NF ++ K

Sbjct: 181 DRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285

DIL+ + F KN KI N Y

Sbjct: 240 TKDILIPSSEAYGKFSKNINFKKIKIKENVY 270

tr Q938X6 Alpha-2,3-/alpha-2,8-sialyltransferase [cstII]  
Q938X6\_CAMJE [Campylobacter  
jejuni]

Score = 287 bits (735), Expect = 4e-76

Identities = 142/271 (52%), Positives = 184/271 (67%), Gaps = 2/27

Query: 16 MQNIIIIAGNGPSLKNINYKRLPREYDVFRNCQFYFEDKYYLGKKIKAVFFNPGVFL  
M+ +II+GNGPSLK I+Y RLP ++DVFRNCQFYFEDKYYLGKK KAVF+NP +F

Sbjct: 1 MKKVIIISGNGPSLKEIDYSRLPNDFDVFRNCQFYFEDKYYLGKKCKAVFYNP SLFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLFPFIESNDFLHQFYNFFPDACLGYEVIENLKEFY  
T K LI EYE + I CS FN +E+ +F+ FY++FPDA LGY+ + LKEF  
Sbjct: 61 TLKHLIQNQEYETELIMCSNFNQAHLENQNFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP  
++EIIYFN+RITSGVYMC +AIALGYK IYL GIDFY+ Y F+ N+ + P  
Sbjct: 121 FHEIYFNQRITSGVYMCTVAIALGYKEIYLSGIDFYQNGSSYAFDTKQKNLLKLAP

Query: 195 DFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK  
D HSK DI+AL+ L+ Y++ +Y LC +S+LAN L+ N+N+NF ++ K  
Sbjct: 181 DNSHYIGHSKNTDIKALEFLEKTYEIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285  
DIL+ + F KN KI N Y  
Sbjct: 240 TKDILIPSSEAYGKFTKNINFKKIKIKENIY 270

tr Q50FZ0 Cj81-011 (Fragment) [Campylobacter jejuni] 2  
Q50FZ0\_CAMJE a

Score = 287 bits (735), Expect = 4e-76

Identities = 142/271 (52%), Positives = 184/271 (67%), Gaps = 2/27

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKY YLGKKIKAVFFNPGVFL  
M+ +IIAGNGPSLK I+Y RLP ++DVFRCNQFYFEDKY YLGKK KAVF+ P F  
Sbjct: 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFRCNQFYFEDKY YLGKKCKAVFYTPNFFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLFPFIESNDFLHQFYNFFPDACLGYEVIENLKEFY  
T K LI EYE + I CS +N +E+ +F+ FY++FPDA LGY+ + LKEF  
Sbjct: 61 TLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP  
++EIIYFN+RITSGVYMCA+AIALGYK IYL GIDFY+ Y F+ N+ + P  
Sbjct: 121 FHEIYFNQRITSGVYMCAVAIALGYKEIYLSGIDFYQNGSSYAFDTKQENLLKLAP

Query: 196 FKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK  
+ HSK DI+AL+ L+ YK+ +Y LC +S+LAN L+ N+N+NF ++ K  
Sbjct: 181 DRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285  
DIL+ + F KN KI N Y  
Sbjct: 240 TKDILIPSSEAYGKFSKNINFKKIKIKENVY 270

tr Q93CZ5 Bifunctional alpha-2,3/-2,8-sialyltransferase [cst-

Q93CZ5\_CAMJE

II]

[Campylobacter jejuni]

Score = 287 bits (734), Expect = 5e-76

Identities = 142/271 (52%), Positives = 185/271 (67%), Gaps = 2/27

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRNCFYFEDKYYLGKKIKAVFFNPGVFL  
M+ +II+GNGPSLK I+Y RLP ++DVFRNCFYFEDKYYLGKK KAVF+NP +F  
Sbjct: 1 MKKVIIISGNGPSLKEIDYSRLPNDFDVFRNCFYFEDKYYLGKKCKAVFYNP SLFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENTLKEFY  
T K LI EYEI+ I CS +N +E+ +F+ FY++FPDA LGY+ + LKEF  
Sbjct: 61 TLKHLIQNQEYEIELIMCSNYNQAHLNENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP  
++EIYFN+RITSGVYMC +AIALGYK IYL GIDFY+ Y F+ N+ + P  
Sbjct: 121 FHEIYFNQRITSGVYMCTVAIALGYKEIYLSGIDFYDNGGGYAFDTKQKNLLKLAP

Query: 195 DFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK  
D HSK DI+AL+ L+ Y++ +Y LC +S+LAN L+ N+N+NF ++ K  
Sbjct: 181 DNSHYIGHSKNTDIKALEFLEKTYEIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285  
DIL+ + F KN KI N Y  
Sbjct: 240 TKDILIPSSEAYGKFTKNINFKKIKIKENIY 270

tr Q93D05  
Q93D05\_CAMJEAlpha-2,3-sialyltransferase [cst-II] [Campylobacter  
jejuni]

Score = 286 bits (731), Expect = 1e-75

Identities = 141/271 (52%), Positives = 183/271 (67%), Gaps = 2/27

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRNCFYFEDKYYLGKKIKAVFFNPGVFL  
M+ +IIAGNGPSLK I+Y RLP ++DVFRNCFYFEDKYYLGKK K VF+ P F  
Sbjct: 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFRNCFYFEDKYYLGKKCKTVFYTPNFFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENTLKEFY  
T K LI EYE + I CS +N +E+ +F+ FY++FPDA LGY+ + LKEF  
Sbjct: 61 TLKHLIQNQEYETELIMCSNYNQAHLNENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP  
++EIYFN+RITSGVYMC+AIALGYK IYL GIDFY+ Y F+ N+ + P  
Sbjct: 121 FHEIYFNQRITSGVYMCAVAIALGYKEIYLSGIDFYQNGSSYAFDTKQENLLKLAP

Query: 196 FKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK  
+ HSK DI+AL+ L+ YK+ +Y LC +S+LAN L+ N+N+NF ++ K

Sbjct: 181 DRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285

DIL+ + F KN KI N Y

Sbjct: 240 TKDILIPSSEAYGKFSSKNINFKKIKIKENVY 270

tr Q7BP25 Hypothetical protein Cj1140 (2,3-sialyl  
Q7BP25\_CAMJE transferase)  
(Alpha-2,3-sialyltransferase) [cstIII]  
[Campylobacter  
jejuni]

Score = 261 bits (667), Expect = 3e-68

Identities = 136/263 (51%), Positives = 182/263 (68%), Gaps = 10/2

Query: 18 NIIIAGNGPSLKNINIKRLPREYDVFRNCFYFEDKYLLGKKIKAVFFNPVFLQQ  
N ++ GNGPSLKNI+YKRLP+++DVFRNCFYFED+Y++GK +K VFFNP VF +Q

Sbjct: 6 NALVCGNGPSLKNIDYKRLPKQFDVFRNCFYFEDRYFVGKDVKYVFFNPVFFFEQ

Query: 78 KQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENLKEFYAY  
K+LI EY I+NI CST NL +I+ F+ F +F DA LG+E+I+ LK+F+AY

Sbjct: 66 KKLIQNEEYNIENIVCSTINLEYIDGFQFVDNFELYFSDAFLGHEIIKKLKDFEAY

Query: 138 EIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEG-DVIYPFEAMSTNIKTIFPG  
EIY +RITSGVYMCA A+ALGYK+IY+ GIDFY+ + +Y F+ N+ G

Sbjct: 126 EIYNRQRITSGVYMCATAVALGYKSIYISGIDFYQDTNNLYAFDNNKKNLLNKCTG

Query: 196 -FKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK  
FK N HS D++AL L Y VNIY+L D +F L+ +I ++F L K

Sbjct: 186 KFKFIN-HSMACDLQALDYLKRYDVNIYSLNSD----EYFKLAPDIGSDFVLSKK

Query: 255 INDILLTDNTPGVSFY--KNQLK 275

INDIL+ D +Y K++LK

Sbjct: 241 INDILIPDKYAQERYYGKKSRLK 263

tr Q32VQ2 Putative glycosyltransferase [Campylobacter jejuni  
Q32VQ2\_CAMJE subsp. jejuni]

Score = 229 bits (585), Expect = 9e-59

Identities = 125/206 (60%), Positives = 143/206 (68%), Gaps = 24/2

Query: 247 LENKHNNNSINDILLTDNTPGV-----SFYKNQLKADNKIMLN  
+ NK+ N++ + LL D + Y ++ + K++ N

Sbjct: 327 IANKYQNTVLENLLNDRISALWQILDCKDPLDILNKIPKKLYIKKVFSLKKVIKN

Query: 288 LHSKDTLIKFLNKEIAVLKKQTT-----QRAKARIQNHLASYKLGQALIINSKSVLG  
L +K T+I +I L K +AK RIQN LSYKLGQALIINSKSVLG  
Sbjct: 387 LENKKTIIINQTNQIHNLNKTlnfQNNYgKAKIRIQNQLSYKLGQALIINSKSVLG

Query: 343 PFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEE  
PFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEE  
Sbjct: 447 PFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEE

Query: 403 GKNWYGEgyIKFIFKdVpRLKREFEK 428  
KNWYG GYIKF FKdVpRLKRE+++  
Sbjct: 507 SKNWYGGGYIKFYFKdVpRLKREYKR 532

tr Q4QM36 CMP-neu5Ac--lipooligosaccharide alpha 2-3  
Q4QM36\_HAEI8 sialyltransferase  
[lic3A2] [Haemophilus influenzae (strain 86-028NP)]

Score = 222 bits (565), Expect = 2e-56  
Identities = 124/248 (50%), Positives = 161/248 (64%), Gaps = 6/24

Query: 17 QNIIIAGNGPSLKNINyKRLPREYDVFRcNQFYFEDKYyLGKKIKAVFFNPGVFLQ  
+++IIAGNG SLK+I+Y LP++YDVFRcNQFYFED Y+LGKKIK VFFN V +  
Sbjct: 32 KSVIIAGNGTSLKSIDYSLLPKDyDVFRcNQFYFEDHYFLGKKIKKVFFNCsvIFE

Query: 77 AKQLILKNEYEIKNIFCSTF-NLPFIESNDfLHQFYnFFPDakLGYEVIENLKEFY  
QLI NEYE +I S+F NL E + + P LG+ ++ L+ F  
Sbjct: 92 FMQLIKNNEYEYADIILSSfLNLGDSELKK-IQRLEKLLPQIDLGHSyLKKLRAFD

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFY-EGDVIYPFEAMSTNIKTIF  
Y+E+Y NKRITSGVYMCA+A A+GYK +YL GIDFY E Y F + NI +  
Sbjct: 151 YHELYENKRITSGVYMCAVATAMGYKDLYLTGIDFYQEKGNPYAFHHQTENIIKLL

Query: 195 DFK-PSNCHSKEYDIEALKLLKSIYKVNIYALCDDSiLANHFPLS-ININNNFTLE  
K S+ HS EYD+ AL L+ Y VNIY + +S L N+FPLS +N F LE  
Sbjct: 211 QNKSQSDIHSMEYDLNAlYFLQKHYGvNIYcISPESPLcNYfPLSPLNNPITFILE

Query: 253 NSINDILL 260  
+ DIL+  
Sbjct: 271 YT-QDILI 277

tr Q32VR2 Putative glycosyltransferase [Campylobacter jejuni  
Q32VR2\_CAMJE subsp. jejuni]

Score = 219 bits (557), Expect = 2e-55

Identities = 146/357 (40%), Positives = 196/357 (54%), Gaps = 35/3

```
Query: 81  ILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYE-----VIENLKEFY
          I+  ++    + C   N  +I  N      Y   P++ + Y      + ++LK F
Sbjct: 242  IIHEDHHFGMLLCLQANKIYINLNKLY--IYRVRPNSIMNYNDNGKNINKSLKNFC

Query: 136  YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNI--KTI
          N I   K      Y      +AL +          +F+  D+I  F      N      I
Sbjct: 300  LNVIDGKKYYKILSYGINAFLALNFSN-----NFHNKDLIKLFNKAFKNECENWI

Query: 194  KDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLEN
          +  ++   S      IE  +++K+ Y+ N   L   D I          ++ INNN
Sbjct: 354  AQYPTNDLRS--LFIEIFRIMKN-YETNYENLILDFI-----AMIINNNKITIV

Query: 254  SINDILLTDNTPGVSFYKNQLKADNKIMLNFYNI LHSKDTLIK-----FLNKEIAV
          I +      N   + Y  ++ + N I+L   N +H+ +T ++      + KE  +
Sbjct: 404  EIQN-----NQNTIKIYCEKINSQNNIILQQTNQIHNLNTTLENKNQLLITKENLL

Query: 309  TTQRAKARIQNHLSYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKV
          +AK R+QN LSYKLGQALI+NSKSVLGFLSLPFIILSI+ISHKQEQKAYKFKV
Sbjct: 459  NYGKAKTRVQNQLSYKLGQALILNSKSVLGFLSLPFIILSIIISHKQEQKAYKFKV

Query: 369  NLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyikFIFKDVPR LKR
          NLALPPLETYPDYNEALKEKECFTYKLGE  I+A KNWYG GYIKF  D+  LKR
Sbjct: 519  NLALPPLETYPDYNEALKEKECFTYKLGEALIQASKNWYGGGYIKFWLIDIQNLKR
```

tr Q5W602 Putative glycosyltransferase [Campylobacter jejuni]  
Q5W602\_CAMJE

Score = 219 bits (557), Expect = 2e-55

Identities = 146/357 (40%), Positives = 196/357 (54%), Gaps = 35/3

```
Query: 81  ILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYE-----VIENLKEFY
          I+  ++    + C   N  +I  N      Y   P++ + Y      + ++LK F
Sbjct: 242  IIHEDHHFGMLLCLQANKIYINLNKLY--IYRVRPNSIMNYNDNGKNINKSLKNFC

Query: 136  YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNI--KTI
          N I   K      Y      +AL +          +F+  D+I  F      N      I
Sbjct: 300  LNVIDGKKYYKILSYGINAFLALNFSN-----NFHNKDLIKLFNKAFKNECENWI

Query: 194  KDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLEN
          +  ++   S      IE  +++K+ Y+ N   L   D I          ++ INNN
Sbjct: 354  AQYPTNDLRS--LFIEIFRIMKN-YETNYENLILDFI-----AMIINNNKITIV
```



Query: 254 SINDILLTDNTPGVSFYKNQLKADNKIMLNFYINILHSDTKLIK-----FLNKEIAV  
I + N + Y ++ + N I+L N +H+ +T ++ + KE +  
Sbjct: 404 EIQN-----NQNTIKIYCEKINSQNNIILQQTNQIHNLNTTLENKNQLLITKENLL

Query: 309 TTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKV  
+AK R+QN LSYKLGQALI+NSKSVLGFLSLPFIILSI+ISHKQEQKAYKFKV  
Sbjct: 459 NYGKAKTRVQNQLSYKLGQALILNSKSVLGFLSLPFIILSIIISHKQEQKAYKFKV

Query: 369 NLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIKFIFKDVPRLLK  
NLALPPLETYPDYNEALKEKECFTYKLG I+A KNWYG GYIKF D+ LKR  
Sbjct: 519 NLALPPLETYPDYNEALKEKECFTYKLGELIQASKNWYGGGYIKFWLIDIQNLKR

tr Q5M6Q2 Putative sugar transferase [HS23.17] [Campylobacter  
Q5M6Q2\_CAMJE jejuni]

Score = 214 bits (546), Expect = 3e-54  
Identities = 122/188 (64%), Positives = 133/188 (69%), Gaps = 20/1

Query: 241 INNNFTLENKHNNI---NDILLTDNTPGVSFYKNQLKADNKIMLNFYINILHSDTK  
I NN T + + N I D +LT T NQ+ N + N +L +K  
Sbjct: 398 IKNNLTQDIYLNQILENKDKILTQT-----NQIYNLNTTLENKNQLLIAKQN

Query: 298 LNKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISH  
N +AK RIQNHLASYKLGQALIINSKSVLG+LSLPFIILSIVISH  
Sbjct: 451 QNNY-----GKAKTRIQNHLASYKLGQALIINSKSVLGYLSLPFIILSIVISH

Query: 358 KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIK  
KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKA KNWYG GYIK  
Sbjct: 502 KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKASKNWYGGGYIK

Query: 418 DVPRLKRE 425  
+ +LKRE  
Sbjct: 562 -IKKLKRE 568

tr Q9CLP3 Hypothetical protein PM1174 [PM1174] [Pasteurella  
Q9CLP3\_PASMU multocida]

Score = 213 bits (542), Expect = 9e-54  
Identities = 117/248 (47%), Positives = 155/248 (62%), Gaps = 8/24

Query: 19 IIIAGNGPSLKNINYKRLPREYDVFRNCQFYFEDKYIYLGKKIKAVFFNPGVFLQY  
+I+AGNG SL I+Y+ LP+ YDVFRNCQFYFE++Y+LG KIKAVFF PGVFL+QY  
Sbjct: 13 VIVAGNGESLSQIDYRLLPKNYDVFRNCQFYFEERYFLGNKIKAVFFTPGVFLEQY

Query: 79 QLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNNFFPDAKLGYE-VIENLKEFYAY  
L NEY + N+ S+FN P ++ + + F D GYE + L F Y  
Sbjct: 73 HLKRNNEYFVDNVILSSFNHTVDL-EKSQKIQALFIDVINGYEKYLSKLTAFDVY

Query: 138 EIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYE-GDVIYPFEAMSTNIKTIFPG  
E+Y N+RITSGVYMCA+AIA+GY IYL GIDFY+ + Y F+ NI + P  
Sbjct: 132 ELYENQRITSGVYMCAVAIAMGYTDIYLTGIDFYQASEENYAFDNKKPNIIRLLPD

Query: 197 KP-SNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSI---NINNNFTLE  
K + HSK+ D+EAL L+ Y VN Y++ S L+ HFP+ + F  
Sbjct: 192 KTLFSYHSKDIDLEALSFLQQHYHVNIFYSISPMSPLSKHFPIPTVEDDCETTFVAP

Query: 253 NSINDILL 260  
N INDILL  
Sbjct: 251 NYINDILL 258

tr Q6EF79 Putative glycosyltransferase [Campylobacter jejuni]  
Q6EF79\_CAMJE

Score = 212 bits (539), Expect = 2e-53

Identities = 120/188 (63%), Positives = 133/188 (69%), Gaps = 20/1

Query: 241 INNFTLENKHNNNSI---NDILLTDNTPGVSFYKNQLKADNKIMLNFYNNILHSKDT  
I NN T + + N I D +LT T NQ+ N + N +L +K  
Sbjct: 398 IKNNLTQDQIYLNQILENKDKILTQT-----NQIYNLNTTLENKNQLLIAKQN

Query: 298 LNKEIAVLKKQTTQRAKARIQNHLSYKLGQALIINSKSVLGFLSLPFIILSIVISH  
N +AK RIQ+HLSYKLGQALIINSKSVLG+LSLPFIILSIVISH  
Sbjct: 451 QNNY-----GKAKTRIQDHLSYKLGQALIINSKSVLGYLSLPFIILSIVISH

Query: 358 KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEFEIKAGKNWYGEgyik  
KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEFEIKA KNWYG GYIK  
Sbjct: 502 KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEFEIKASKNWWYGGGYIK

Query: 418 DVPRLKRE 425  
+ +LKRE  
Sbjct: 562 -IKKLKRE 568

tr Q4QNI8 CMP-Neu5Ac--lipooligosaccharide alpha 2-3 sialyltransferase  
Q4QNI8\_HAEI8 [lic3A]  
[Haemophilus influenzae (strain 86-028NP)]

Score = 211 bits (538), Expect = 3e-53

Identities = 124/279 (44%), Positives = 161/279 (57%), Gaps = 8/27

Query: 17 QNIIIAGNGPSLKNINYKRLPREYDVFRNCNQFYFEDKYYLGKKIKAVFFNPGVFLQ  
+++IIAGNG SLK+I+Y LP++YDVFRNCNQFYFED Y+LGKKIK VFFN V +

Sbjct: 27 KSVIIAGNGTSLKSIDYSLLPKDYDVFRNCNQFYFEDHYFLGKKIKKVFFNCSVIFE

Query: 77 AKQLILKNEYEIKN---IFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENTLKE  
QLI NEY+ + I S NL H P LG+ ++ L+

Sbjct: 87 FMQLIKNNEYKYEYADIILASFLNLGDSTLKKIQH-LEKLLPQIDLGHCYLKKLRA

Query: 134 IKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFY-EGDVIYPFEAMSTNIKT  
++Y+E+Y NKRITSGVYMCA+A A+GYK +YL GIDFY E Y F NI

Sbjct: 146 LQYHELYENKRITSGVYMCAVATAMGYKDLYLTLGIDFYQEKGPNPYAFHHQKENIIK

Query: 193 IKDFK-PSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTL  
K S+ HS EYD+ AL L+ Y VNIY + +S L N+FPLS N +

Sbjct: 206 FSQNKSQSDIHSMEYDLNALYFLQKHVYGVNIYCISPESPLCNFYFPLSPLNNPIAFI

Query: 252 NNSINDILLTDN--TPGVSFYKNQLKADNKIMLNFYNIL 288

N DIL+ + Y N I F++IL

Sbjct: 266 KNYTQDILIPPKFVYKKIGIYSKPRIYQNLIFRLFWDIL 304

tr Q6EF56 Putative glycosyltransferase [Campylobacter jejuni]  
Q6EF56\_CAMJE

Score = 207 bits (527), Expect = 5e-52

Identities = 119/188 (63%), Positives = 130/188 (68%), Gaps = 20/1

Query: 241 INNNFTLENKHNSI---NDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSKDT  
I NN T + + N I D +LT T NQ+ N + N +L +K

Sbjct: 398 IKNNLTQDQIYLNQILENKDKILTQT-----NQIYNLNTTLENKNQLLIAKQN

Query: 298 LNKEIAVLKKQTTQRAKARIQNHLASYKLQALIINSKSVLGFLSLPFIILSIVISH  
N AKARIQNHLASYKLQALIINSKSVLG+LSLPFIILSIVISH

Sbjct: 451 QNHY-----GTAKARIQNHLASYKLQALIINSKSVLGYLSLPFIILSIVISH

Query: 358 KAYKFKVKNPNLALPPLETYPDYNEALKEKECFTYKLGEFFIKAGKNWYGEGYIK  
KAYKFKV KNPALPPL YPDYNEALKEKECFTYKLGEFFIKA KNWYG GYIK

Sbjct: 502 KAYKFKVKNPNLALPPLVAYPDYNEALKEKECFTYKLGEFFIKASKNWWYGGGYIK

Query: 418 DVPRLKRE 425

+ +LKRE

Sbjct: 562 -IKCLKRE 568

tr Q5W603 Hypothetical protein [Campylobacter jejuni] 3  
Q5W603\_CAMJE a

Score = 207 bits (526), Expect = 7e-52

Identities = 121/217 (55%), Positives = 140/217 (63%), Gaps = 35/2

Query: 205 EYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLE-----NKH  
+YD+E YK +IY D L N + + + N +E NK

Sbjct: 197 DYDLE-----YKESIYKNLDVQFLLNMYKEKL-FSKNKEIEKLRLSQFKKNKE

Query: 256 NDILLTDNTPGVSFYK NQLKADNKIMLN FYNILH SKDTLIKFLNKEIAVLKKQTTQ  
N+I+L NQ+ N + N +L +K+ L+ F N

Sbjct: 248 NNIIILQQT-----NQIHNLTNTLENKNQLLITKENLLNFQNNY-----G

Query: 316 RIQNHLSYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA  
R+QN LSYKLGQALI+NSKSVLGFLSLPFIILSI+ISHKQEQKAYKFKVKKNPNLA

Sbjct: 291 RVQNQLSYKLGQALILNSKSVLGFLSLPFIILSIIISHKQEQKAYKFKVKKNPNLA

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyI 412  
ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYG G I

Sbjct: 351 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGGGII 387

tr Q32VQ8 Hypothetical protein [Campylobacter jejuni subsp.  
Q32VQ8\_CAMJE jejuni]

Score = 199 bits (506), Expect = 1e-49

Identities = 144/390 (36%), Positives = 194/390 (48%), Gaps = 79/3

Query: 81 ILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFP-DAKLGYEVIENLKEFYAYIK  
I +N ++ KNI +FN +N+ + F + F + ++ +E + E +

Sbjct: 155 IYENVFKHKNI I IKSFNKDKFLNNNLIDDFLSIFKINRDSSFKTMETMNESLDIL-

Query: 140 YFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTI---FPG  
G+ +C I D D+I + + +K + F

Sbjct: 210 -----GINICNILYE-----DKNFSDLIIEKNLIPSFVKIMEKFFST

Query: 197 KPSNCHSKEYDIEALKLLKSIYK--VNIYALCDDSI LANHFPLSININNNFTLENK  
P Y++ K +K + +N AL FP ININ + K

Sbjct: 251 LPKKTIYNNYNLFYNKEIKELENRYLNGQAL-----FP-PININ-----KYK

Query: 255 INDILLTDNTPGVSFYK-----NQLKADNKIMLN FYNILH SKDTLIKFLNK  
IN+I D + F+K NQ NK N N K +++ N

Sbjct: 296 INEIKHDDFKQIILFFKEIITLILTFQNNQIQKNKEFQNIANSFPLKKQILELANL

Query: 305 LKKQTTQR-----AKARIQNHLSYKLGQALIINSKSV

```
      + K+      +      AKARIQNHLASYKLGQALI NSKS+
Sbjct: 356 IIKKLESKKLAKSLGLKMSIINPKITFIQANS AKARIQNHLASYKLGQALIAN SKSI

Query: 341 SLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLG
      +P+++ I   HK EQKAY+ K+K+NPNLALPPLETYPDYNEALKEKECFTYKLG
Sbjct: 416 RIPYVLSYIKDKHKFEQKAYEEKIKENPNLALPPLETYPDYNEALKEKECFTYKLG

Query: 401 KAGKNWYGEgyikFIFKDVPRlkREFEKGE 430
      +A KNWYG GYIKFIFKDVPRlkREFEKGE
Sbjct: 476 QANKNWYGGgyikFIFKDVPRlkREFEKGE 505
```

```
tr   Q32VR3      Hypothetical protein [Campylobacter jejuni subsp.
      Q32VR3_CAMJE      jejuni]
```

Score = 197 bits (501), Expect = 5e-49

Identities = 116/215 (53%), Positives = 136/215 (62%), Gaps = 35/2

```
Query: 205 EYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLE-----NKH
      +YD+E      YK +IY   D   L N +   +   + N +E      NK
Sbjct: 197 DYDLE-----YKESIYKNLDVQFLLNMYKEKL-FSKNKEIEKLRLSQFKKNKE

Query: 256 NDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSDTLIKFLNKEIAVLKKQTTQ
      N+I+L      NQ+   N   + N   +L +K+ L+ F N
Sbjct: 248 NNIILQQT-----NQIHNLNTTLENKNQLLITKENLLNFQNNY-----G

Query: 316 RIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA
      R+QN LSYKLGQALI+NSKSVLGFLSLPFIILSI+ISHKQEQKAYKFKVKKNPNLA
Sbjct: 291 RVQNQLSYKLGQALIILNSKSVLGFLSLPFIILSIIISHKQEQKAYKFKVKKNPNLA

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEg 410
      ETYPDYNEALKEKECFTYKLGE I+A KNWYG G
Sbjct: 351 ETYPDYNEALKEKECFTYKLGEALIQASKNWYGGG 385
```

```
tr   Q32VQ3      Hypothetical protein [Campylobacter jejuni subsp.
      Q32VQ3_CAMJE      jejuni]
```

Score = 197 bits (500), Expect = 7e-49

Identities = 106/156 (67%), Positives = 117/156 (74%), Gaps = 10/1

```
Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSDTLIKFLNKEIAVLKKQTT
      I DI+ T+N   +      L+ N+ + N   N +H+ +   + F N
Sbjct: 326 IADI IKTNNE-NILGLNQTL EIKNQELRNQTNQIHNLNKT LNFQNNY-----
```

Query: 315 ARIQNHLASYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNL  
RIQN LSYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNL  
Sbjct: 376 IRIQNQLSYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNL

Query: 375 LETYDPDYNEALKEKECFTYKLGEEFIKAGKNWYGE 410  
LETYDPDYNEALKEKECFTYKLGEEFIK KNWYG G  
Sbjct: 436 LETYDPDYNEALKEKECFTYKLGEEFIKASKKNWYGG 471

tr Q5HT01 Capsular polysaccharide biosynthesis protein,  
Q5HT01\_CAMJR putative [CJE1603]  
[Campylobacter jejuni (strain RM1221)]

Score = 171 bits (434), Expect = 3e-41  
Identities = 87/161 (54%), Positives = 115/161 (71%), Gaps = 9/161

Query: 271 KNQLKADNKIMLNIFYNILHSDTLIKFLNKEIAVLKKQTTQRAKARIQNHLASYKLG  
K Q K DNK + F + + + K+ ++ A R++NHL YK G  
Sbjct: 493 KLGKVDNKKLNRF-----EYFFQEIMKKYKGIENNVYLSALQVRNHLCYKFG

Query: 331 INSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYDPDYNEALK  
NSKS+LG++ +P+++ I HKQEQKAY+ K+K+NPALPPLETYDPDYNEALK  
Sbjct: 546 ENSKSILGYIRMPYVLSHIKDKHKQEQKAYEEKIKENPNLALPPLETYDPDYNEALK

Query: 391 FTYKLGEEFIKAGKNWYGEYIKFIFKDVPRKRE-FEKGE 430  
FTYKLG+EFIKA +NWYG GYIK +F ++ RLK+E ++KG+  
Sbjct: 606 FTYKLGQEFIKASQNWYGGGYIKLLF-EIRRLKKEYYDKGK 645

tr Q5M6U5 Putative sugar transferase [HS41.06] [Campylobacter  
Q5M6U5\_CAMJE jejuni]

Score = 167 bits (422), Expect = 8e-40  
Identities = 101/215 (46%), Positives = 126/215 (57%), Gaps = 18/2

Query: 204 KEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININ---NNFTLENKHNNSI  
KEY+ L +YK I C PL I+ L+NK N +  
Sbjct: 368 KEYNFNHLIPPVELYKEIIDEYCTVMDPVKLAPLQKQISALTQEKQDLQNKQFQNEL

Query: 260 LTDNTPGVSFYKNQLKADNKIMLNIFYNILHSDTLIKFLNKEIAVLKKQTT---Q  
+ K L+ N L SK L K L +++++ + T  
Sbjct: 428 VK-----KQHLELTNLEQDLIIKKLESKK-LAKSLGLKMSIINPRITFIQAN

Query: 316 RIQNHLASYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA  
RIQNHLASYKLGQALI NSKS+LG++ +P+++ I H+ EQKAY+ K+K+NPALA

Sbjct: 478 RIQNHLSYKLGQALITNSKSILGYIRMPYVLSYIKDKHQLEQKAYEEKIKENPNLA

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYEGG 410  
ETYPDYNEALKEKECFTYKLG FIKAGKNWY G

Sbjct: 538 ETYPDYNEALKEKECFTYKLGFAFIKAGKNWYRGG 572

tr Q6EBB5 Tgh007 (Fragment) [Campylobacter jejuni] 1.  
Q6EBB5\_CAMJE a.

Score = 160 bits (404), Expect = 9e-38  
Identities = 79/120 (65%), Positives = 93/120 (76%), Gaps = 1/120

Query: 308 QTTQRAKARIQNHLSYKLGQALIINSSVLFSLPFIILSIVISHKQEQKAYKFK  
+T AK RIQN L Y+LGQA+IINSK+ LG++ LP+I+LSIVI +KQEQK YK K  
Sbjct: 9 KTFSTAKQRIQNQLPYRLGQAMIINSKNFLGYIFLPYILLSIVILYKQEQKNYKHK

Query: 368 PNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyikFIFKDVPRLK  
P LPPLETYPDYNEALKEK CFTYKLG I+A K WYG GYIK FK + +LK  
Sbjct: 69 PESTLPPLETYPDYNEALKEKRCFTYKLGALALIEANKKWWYGGYIKLWFK-IKKLLK

tr Q4HEK5 Alpha-2,3-sialyltransferase [CC01544] [Campylobacter  
Q4HEK5\_CAMCO coli RM2228]

Score = 155 bits (391), Expect = 3e-36  
Identities = 74/116 (63%), Positives = 91/116 (77%), Gaps = 1/116

Query: 313 AKARIQNHLSYKLGQALIINSSVLFSLPFIILSIVISHKQEQKAYKFKVKKNP  
AK RIQN LSYKLGQA+I NSKS+LG++ +PF++ I HKQEQK Y+ K+KK+P  
Sbjct: 58 AKTRIQNQLSYKLGQAMITNSKSLGYYIRMPFVLSYIHDKHKQEQKIYQEKIKKDP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyikFIFKDVPRLKREFEK  
PPLE YPDY EALKEKEC TYKLGE IKA K WY GY+K F ++ +LKREF++  
Sbjct: 118 PPLENYPDYKEALKEKECLTYKLGEALIKANKTWYKGGYVKMWF-EIGKLKREFKE

tr Q4HEL4 Alpha-2,3-sialyltransferase [CC01527] [Campylobacter  
Q4HEL4\_CAMCO coli RM2228]

Score = 153 bits (387), Expect = 9e-36  
Identities = 75/146 (51%), Positives = 101/146 (68%), Gaps = 1/146

Query: 285 YNILHSKDTLIKFLNKEIAVLKKQTTQRAKARIQNHLSYKLGQALIINSSVLFGL

++I D + ++L + +A AK RIQN LSYKLGQA+I NSKS+LG++  
Sbjct: 212 FDIARPCDMISQYLLQGVAKQHVNNGYSAKTRIQNQLSYKLGQAMITNSKSLGYI  
Query: 345 IILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFI  
++ I HKQEQK Y+ K+KK+P+L LPLE YPDY EALKEKEC TYKLGE I  
Sbjct: 272 VLSYIKDKHKQEQKNYQEKIKKDP SLKLPLENYPDYKEALKEKECLTYKLGEALI  
Query: 405 NWYGEgyikFIFKDVPRLKREFEKGE 430  
WY GY+K F ++ +L++ + + E  
Sbjct: 332 TWYKGGYVKMWF-EIGKLRKRYRERE 356

tr Q4HEJ9 Alpha-2,3-sialyltransferase [CC01538] [Campylobacter  
Q4HEJ9\_CAMCO coli RM2228]

Score = 145 bits (366), Expect = 2e-33  
Identities = 116/380 (30%), Positives = 178/380 (46%), Gaps = 40/3

Query: 41 DVFRCNQFYFEDKYYLGKKIKAVFFNPGVFLQQYHTAKQLILKNEYE-IKNIFCST  
++ N F F+ KY K + + G F + L N+++ I NI  
Sbjct: 112 EILSKNHFSFQYKYLCDKNMNILVNFIFGKFEK-----LDNDFKKILNILRRK

Query: 100 FIESNDFLH--QFYNFFPDALGYEVIENLKEFYAYIKYNEIYFNKRITSGVYMCA  
I + L+ +YN K+ E+ + E + Y ++ YFN I +Y+  
Sbjct: 163 HINKSKHLNRYDYNS-QTYKIIREIYRDDFEIFDYDLEDKKYFN--IPQNIYLNN

Query: 158 LGYKTIYLCGIDFYEGDVIYPF-EAMSTNIKTIFPGIKDFKPSNCHSKEYDIEALK  
+ K I L + + I + + T KTI + N + + +  
Sbjct: 220 ILIKNINLDSLRLKKS FQIQNLNQT IETKNKTIQENLSQINN LNQT IETKNKTIQE

Query: 217 IYKVNIYALCDD SILANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVSFYKN  
I +N + + + N+N +NK + +N ++  
Sbjct: 280 INN LNQT IETKNKTIQENLSQINN LNQT IETKNK-----TIQENLSQINN LNQ

Query: 277 DNKIMLNFYNIHLSKDTLIKFLNKEIAVLKKQTTQRAKARIQNHL SYKLGQALIIN  
NK + N KD L+ F + AK+RIQN LSYKLGQ +I+N  
Sbjct: 332 KNKTIQN-----KDDLNF-----QAQYGTAKSRIQNQLSYKLGQTMIVN

Query: 337 LGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFT  
LG L +P I+L IVISHKQEQK YK K++K+P+L LP LE YPDY EA+K K +  
Sbjct: 376 LGCLLMPVILLGIVISHKQEQKIYKQKIEKDPSLKLPSLEQYPDYREAIKLNHLS

Query: 397 EEFIKAGKNWYGEgyikFIF 416  
+E +KA K WY GY +F++  
Sbjct: 436 KELVKANKIWKGGYFQFLY 455



sp P24324 Hypothetical protein HI0352 (ORF1) [HI0352] 2  
Y352\_HAEIN [Haemophilus 2  
influenzae]

Score = 129 bits (324), Expect = 2e-28

Identities = 82/186 (44%), Positives = 104/186 (55%), Gaps = 6/186

Query: 79 QLILKNEYEIKNIFCSTF-NLPFIESNDFLHQFYNFFPDAKLGYEVIENLKEFYAY  
QLI NEYE +I S+F NL E + +G+ + L F AY

Sbjct: 2 QLIKNEYEYADIILSSFVNLGDSELKK-IKNVQKLLTQVDIGHYYLNKLPAFDAY

Query: 138 EIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFY-EGDVIYPFEAMSTNIKTIFPG  
E+Y NKRITSGVYMCA+A +GYK +YL GIDFY E Y F NI + P

Sbjct: 61 ELYENKRITSGVYMCAVATVMGYKDLYLTGIDFYQEKGNPYAFHHQKENIIKLLPS

Query: 197 K-PSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLS-ININNNFTLENK  
K S+ HS EYD+ AL L+ Y VNIY + +S L N+FPPLS +N F LE K

Sbjct: 121 KSQSDIHSMEYDLNALYFLQKHVGVNIYCISPESPLCNFYFPLSPLNNPITFILEEK

Query: 255 INDILL 260

DIL+

Sbjct: 181 -QDILI 185

tr Q5M6M2 Putative sugar transferase [HS19.11] [Campylobacter  
Q5M6M2\_CAMJE jejuni]

Score = 124 bits (310), Expect = 7e-27

Identities = 68/151 (45%), Positives = 93/151 (61%), Gaps = 4/151

Query: 270 YKNQLKADNKIMLNIFYNILHSKDTLIKFLNKEIAVLKKQTTQR----AKARIQNHL  
YK+ L + K+ + + I D + F+N + K Q AK RIQN L

Sbjct: 346 YKDILFENIKLNQDPWAIKDKIDIINFFVNNKFKDNKYQFNTNLYGTAKQRIQNQL

Query: 326 GQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDY  
GQ +IINSKS++G L +P +LS +++KQ+QK Y K+KK+P L LPPL E YPDY

Sbjct: 406 GQTMIIINSKSIIGILFMPYIYLLSTFLNYKQDQKIYHQKIKKDPTLKLPLENYPDY

Query: 386 KEKECFYTYKLGEFIKAGKNWYGEFYIKFIF 416

K KE +YKLG+ +++ K W+ G KF F

Sbjct: 466 KYKEHLSYKLGKILLESFKTWHKGGFLFKFPF 496

tr Q5M6M5 Putative sugar transferase [HS19.08] [Campylobacter  
Q5M6M5\_CAMJE jejuni]

Score = 122 bits (306), Expect = 2e-26  
Identities = 58/104 (55%), Positives = 75/104 (71%)

Query: 313 AKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNP  
AK RIQN L YKLGQ +IINSKS++G L +P +LS +++KQ+QK Y K+KK+P  
Sbjct: 390 AKQRIQNQLCYKLGQTMIIINSKSIIGILFMPPIYLLSTFLNYKQDQKIYHQIKKDP  
  
Query: 373 PPLETPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIKFIF 416  
PPLE YPDY EALK KE +YKLG+ +++ K W+ G KF F  
Sbjct: 450 PPLENYPDYQEALKYKEHLSYKLGKILLESFKTWHKGGFLFKFPF 493

tr Q5HT02 Capsular polysaccharide biosynthesis protein,  
Q5HT02\_CAMJR putative [CJE1602]  
[Campylobacter jejuni (strain RM1221)]

Score = 120 bits (301), Expect = 8e-26  
Identities = 66/197 (33%), Positives = 111/197 (55%), Gaps = 24/19

Query: 240 NINNNFTLENKHNNNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSDKT--  
+I NF +E+++ + N ++ D ++ L+ N+ DT  
Sbjct: 450 SIKPNFKIEHRYTKAQNGYIMPD-----ISKELYLDLLNLRDKFDTKK  
  
Query: 298 LNKEIAVLKKQTTQR-----AKARIQNHLASYKLGQALIINSKSVLGFLSLPFI  
+ V KK ++ AK+RI+NHL+Y+ G +I S+++LG++ +PFI  
Sbjct: 497 IYFFQKVTKKYCKEKLTDVYFSAKSRIKNHLAYQFGLTMIQYSRNILGYVKMPFI  
  
Query: 350 VISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKN  
++ ++K Y ++ +NP LP ++ Y DY EA+K KE TY+LG+ I+A KN  
Sbjct: 557 FRQYQNKKKEYYERISENPKFILPKIKEYADYQEAIKLKESITYRLGQALIQANKN  
  
Query: 410 GYIKFIFKDVPRCLKREF 426  
GYIK +F ++ RLK+E+  
Sbjct: 617 GYIKLLF-EIRRLKKEY 632

tr Q4HR89 Hypothetical protein [CUP1274] [Campylobacter  
Q4HR89\_CAMUP upsaliensis RM3195]

Score = 115 bits (287), Expect = 3e-24  
Identities = 72/196 (36%), Positives = 109/196 (54%), Gaps = 22/19

Query: 241 INNNFTLENKHNNNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSDKDTLIK  
IN + LE K ++L +N + ++KA K+ L +++ L+K  
Sbjct: 190 INKAYELEQK-----TGVVLKNNKEEKILQ-KIKAQEKL-----LRTQNLLLK

Query: 301 EI-----AVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILS  
+ A + Q + A R+ HL+YKLG A+I+ SKS+LG+ +PF++  
Sbjct: 237 QAKPNNPSPQAQIPLQKPKGAVERVHRHLAYKLGIAIIVCSKSLGAYRMPFVLYH

Query: 353 HKQEQQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYG  
HK EQ+ ++ + KNP L L PLE+Y DY ALKE+ C+TYKLG ++A +N +  
Sbjct: 297 HKFEQEKFKALLKNPTLKLPLESYADYENALKEQRCYTYKLGGLAMMEAHRNLFK

Query: 413 KFIFKDVPRLLKREFEK 428  
F F+ RLKREFEK  
Sbjct: 357 WIFYFES-KRLKREFEK 371

tr Q4HEL1 DcbE, putative [CC01537] [Campylobacter coli  
Q4HEL1\_CAMCO RM2228]

Score = 107 bits (266), Expect = 9e-22  
Identities = 65/143 (45%), Positives = 88/143 (61%), Gaps = 14/143

Query: 274 LKADNKIMLNF-YNILHSDKDTL-----IKFLNKEIAVLKKQTTQRAKARIQ  
LK+ NK +L+F ++I + L IK N ++ K T AK RIQ  
Sbjct: 247 LKSKNKSLLDFFIDIQEDLEKLHQENCRLEAHKNQNSLLSFCMKYGT--AKQRIQ

Query: 323 YKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQQKAYKFKVKKNPNLALPPLETY  
Y+LGQ IINSK++ L +P +LS +IS KQE++ Y K+KK+P+L LPPLE Y  
Sbjct: 305 YRLGQT-IINSKNIFKILFMPIFLLSNIISFKQERQVYNKKIKKDPSSLILPPLEKY

Query: 383 EALKEKECFTYKLGEEFIKAGKN 405  
EA+K K +Y+LG+ IK KN  
Sbjct: 364 EAIKFKNYLSYRLGQVVIKGFKN 386

Score = 34.7 bits (78), Expect = 5.8  
Identities = 15/51 (29%), Positives = 30/51 (58%)

Query: 305 LKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQ 355  
L+K + + +N+LSY+LGQ +I K+ L + LP+ I+ ++ ++  
Sbjct: 356 LEKYPDYQEAIKFKNYLSYRLGQVVIKGFKNPLSIILLPYEIVKLIYKFRK 406

tr Q9PMM6 Hypothetical protein Cj1431c [Cj1431c]  
Q9PMM6\_CAMJE [Campylobacter jejuni]

Score = 99.4 bits (246), Expect = 2e-19

Identities = 63/148 (42%), Positives = 88/148 (58%), Gaps = 13/148

Query: 283 NFYNILHSKDTLIKFLNKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLG  
NF+ I+ D F+ K++ K A +I+NHL+YKLG A I NSKS+ G

Sbjct: 448 NFHPIIF--DQFKMFIFKDLP--KSDQEIGAVKKIRNHLAYKLGVAAIKNSKSLWG

Query: 343 PFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEE  
P+++ I HK+ Q KK+ +L E Y DY ALKEKE F YKLG+

Sbjct: 504 PYVLSYIRDMHKESQNKMD---KKSISL-----EYYS DYESALKEKEGFVYKLGQI

Query: 403 GKNWYGEgyIKFIFKDVPRCLKREFEKGE 430

KNW+ GYI F +V +LK+EF+KG+

Sbjct: 556 HKNWHKGGYIMLWF-EVKKLKKEFKKGK 582

tr Q50FV9 Cj81-063 (Fragment) [Campylobacter jejuni] 56 A  
Q50FV9\_CAMJE align

Score = 99.0 bits (245), Expect = 3e-19

Identities = 47/56 (83%), Positives = 49/56 (86%), Gaps = 1/56 (1%)

Query: 370 LALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPRCLKRE  
LALPPLETYPDYNEALKEKECFTYKLGEEFIKA KNWYG GYIK K + +LKRE

Sbjct: 1 LALPPLETYPDYNEALKEKECFTYKLGEEFIKASKNWYGGGYIKLRLK-IKKLKRE

tr Q4HR98 Hypothetical protein [CUP1265] [Campylobacter  
Q4HR98\_CAMUP upsaliensis RM3195]

Score = 97.1 bits (240), Expect = 1e-18

Identities = 49/116 (42%), Positives = 76/116 (65%), Gaps = 9/116

Query: 311 QRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKK  
Q A +++HL+YKLG +I NSKS+LG + +P+++++I +H +E+K +

Sbjct: 447 QGAIKLVKSHLAYKLGACMIRNSKSLGCIKMPYLLVAIKWAHAERKNF-----

Query: 371 ALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPRCLKREF  
+ PL+ Y DY EALK KE +YKLGE IKA KN + G IKF+FK+ ++R+F

Sbjct: 498 NITPLQDYIDYEEALKVKEFLSYKLGEALIKAYKNMWKGGLIKFVFKEAWEIRRDF

tr Q4HKU2 Glycosyl transferase family 8 family [CLA1010] [Campylobacter  
Q4HKU2\_CAMLA lari  
RM2100]

Score = 90.9 bits (224), Expect = 7e-17

Identities = 50/122 (40%), Positives = 73/122 (58%), Gaps = 6/122

Query: 307 KQTTQRAKARIQNHLASYKLGQALIINSSVGLGFLSLPFIILSIVISHKQEQKAYKF  
KQ+ QR K HLSYKLG A I +K+ LPF +L I H + K Y+

Sbjct: 281 KQSIQRTKY----HLSYKLGAFIECTKNKKKIPFLPFTLLKIYYKHTKLAKQYQK

Query: 367 NPNLALPPLETYPDY-NEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPR  
P L LPPL +Y DY +E +K + ++YK+G+ IKA +NW+ GY+KFI K++

Sbjct: 337 KPYLKLPLSSYDDYKSEGIKNQNTYSYKIGQALIKAQRNWHKGGYVKFI-KELKH

Query: 426 FE 427

++

Sbjct: 396 YK 397

tr Q5M6U6 Putative sugar transferase [HS41.05] [Campylobacter  
Q5M6U6\_CAMJE jejuni]

Score = 89.7 bits (221), Expect = 2e-16

Identities = 46/112 (41%), Positives = 73/112 (65%), Gaps = 1/112

Query: 316 RIQNHLASYKLGQALIINSSVGLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNL  
R++NHL+YKLGQ +I + + G+++L + I HK+EQK YK ++ P L

Sbjct: 10 RVKNHLAYKLGQVMIDFANNGGGYIALFKKLYKIKKQHKKEQKIYKQTIQVFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPRLKREFE 427

ET PDY+E+L+ K +Y LGE IKA N + +GY F+FK++ + K++++

Sbjct: 70 ETCPDYSESLRYKFHLSYMLGEVLIKADMNKFKDGYF-FLFKNIEQTKKDYK 120

tr Q5M6S8 Putative sugar transferase [HS41.23] [Campylobacter  
Q5M6S8\_CAMJE jejuni]

Score = 89.4 bits (220), Expect = 2e-16

Identities = 64/214 (29%), Positives = 107/214 (49%), Gaps = 31/21

Query: 201 CHSKEYDIEALKLLKSIYKV-----NIYALCDDSI LANHFPLSININNNFTL  
C+SKE +A K +K ++ N+Y+ DD ++

Sbjct: 247 CYSKEEFKAFKKIKILHYTYLYMPKPWENVYSFIDDDYNLVYY-----

Query: 252 NNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNIHLSKDTLIKFLNKEI----A  
++ D+ L G F K + + + K +L + + K IK L K+

Sbjct: 293 YDAWWDMAKTPPIYGEHFAKKKREYEKSLTYAQAMSK---IKALEKKTENN

Query: 308 QTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFK  
T A R++NHL+YK+G+ LI N +VL L +PF ++ +++ HK YK  
Sbjct: 350 CLTNGACDRVKNHNLNYKIGRVLIDNF-TVLKILLIPFKLIYVIMIHKISSFIYKIL

Query: 368 PNLALPPLETYPDYNEALKEKECFTYKLGEEFIK 401  
P+L L PLE Y DY EA++ K F+Y+LG+ F+K  
Sbjct: 409 PSLKLLPLEKYADYEEAMRIKSFFSYRLGKLFLK 442

tr Q6EF57 Putative glycosyltransferase (Putative sugar transferase)  
Q6EF57\_CAMJE [HS23.16]  
[Campylobacter jejuni]

Score = 85.1 bits (209), Expect = 4e-15  
Identities = 74/222 (33%), Positives = 105/222 (46%), Gaps = 27/22

Query: 214 LKSIYKVNIYALCDDSI LANHFPLSININNNFTLENKHNNNSI----NDILLT---D  
+K + K IY L +D H + NN F + ++ + I DI L+  
Sbjct: 359 IKYLKKALIYDLNDNDKYRI-HIIYMLLCNNKFKILERYLSIIMSyrKDIFLSTLFS

Query: 267 VSFYKNQLKADNKIMLNFYNILHskDTLIKFLNKEIAVLKKQTTQRAKARIQNHLs  
Y N L YNI + + + I + A ++ Hls  
Sbjct: 418 GYVYLNILSDFLNYSQRIYNIKYLYPNIFYIITEIIKL-----NLFAVFLVKQHLS

Query: 327 QALIINSKSVLGFLSLPFIILSIVISHKQEQKA-YKFKVKKNPNLALPPLETYPDY  
+ I+ +KS+L + LP + +IV SHK+ Q Y K+ E DY  
Sbjct: 473 KR-IVQTKSILDIIELPLDLKNIVDSHKRNQLIPYNIKI-----ENCLDY

Query: 386 KEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPRLKREFE 427  
K K F+YKLG IKA KNWY GYIKF F D+ +LK+E++  
Sbjct: 521 KIKNYFSYKLGLILIKAHKNWYKGGYIKFWF-DLYKLKKEYK 561

tr Q4HR96 Glycosyl transferase, group 2 family protein  
Q4HR96\_CAMUP [CUP1267]  
[Campylobacter upsaliensis RM3195]

Score = 85.1 bits (209), Expect = 4e-15  
Identities = 52/143 (36%), Positives = 81/143 (56%), Gaps = 10/143

Query: 287 ILHskDTLIKFLNKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSL  
IL+SK + + + + K A RI+N LSYKLG+A I+ + S L FL L  
Sbjct: 336 ILNSKkdPLNLVRECVKIQKYIKENGaidRIKNQLSYKLGEA-ILKANSPLKFLKL

Query: 347 LSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKA

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      +S+  +H+  EQK  +F  ++  P      LE Y DY EAL+ K+  +Y+LG+  +K
Sbjct: 395 ISLAKTHQFEQKVLQFLIRLEPKFKPLDLEKYADYEEALRIKKHLSYRLGQALLK-

Query: 407 YGEGYIKFIFKDVPRLLKREFEKG 429
      + FIFK +P + + F+KG
Sbjct: 450 ---NPLTFIFK-IPSIYQNFKKG 468

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tr   Q4HLH9          Hypothetical protein [CLA0678] [Campylobacter lari
     Q4HLH9_CAMLA    RM2100]

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Score = 84.0 bits (206), Expect = 8e-15

Identities = 120/485 (24%), Positives = 198/485 (40%), Gaps = 81/4

```

Query: 4   TRMENELIVSKNMQNI IIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKY YLGKK
          T ++N   + ++ + II +   S  NIN   P   +   N  YF ++ Y   K
Sbjct: 37  TSLQONLYELMRHEKTIKSDFIISESNINDYLSPM SLSIILRNIDYFYEELYKANK

Query: 64  FFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNL PFI E---SND FLHQF---YNF
          P   +   +   + I  NE  KN   FNL  ++   + L+ F   Y  F
Sbjct: 97  LILP---IPACNDKSKAI--NEAHRKN CAYYG FN LIDVDLYYQKNNLYDFDQNYKF

Query: 118  ----KLG YEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCG--
          +LG  +I+NL  F   K  E   +   ++  + +  + +K  + C
Sbjct: 152  LAMQELGKNIIKNLHNFK---KSKENIICSKRKYHIFTPSNSTKIEHKNSFFCEKI

Query: 170  FYEGDVIYPFEAMSTNIKTIFPGIKDFKPSNCH---SKEYDIEALKLLKSIYKVNI
          E  +I+P E   I  I   +   S+ H   S   + KL+K+   +N
Sbjct: 209  ASE-KIIFPKELKGHQILGIHTW--NHASSSTHAISSISIKNSSFKLVKNFGLINT

Query: 224  ----ALCDDS-----ILANHFPLSININNNFT-----LENKHNN
          A+CD+   I  +   ++I N  T   LEN  ++
Sbjct: 266  QNEKAICDEQTFLYINTQIIKQSEESSGLSIANEKTPRLDYVDLIGILLLENDNDK

Query: 258  ILLTDNT-----PGVSFYKNQLKADNKIM-LNFYNILH SKD-TLIKFLNK-----
          NT   P ++FYK  +   +++  L+   L S++  L++FLN
Sbjct: 326  KNYLTNTHELLIPPIAFYKELVLEYHELKKLDMQTFLQSQNHNLRLFLNHKGLKNE

Query: 304  VLKKQTTQRAKARIQNHL SYKLGQALIINSKSVLGFLSLPFIILSIVISHKQE QKA
          + +   A  RI+  LSYKLG+A++ NSKS LG+  +PF  +   +  H  + QK
Sbjct: 386  IHQNNKLYGASLRIKERLSYKLG EAIMKNSKSYLGYFKIPFELRKVKKEHFKNQKD

Query: 364  VKKNPNLALPPLETYPDYNEALKEKECF TYKLGE EFIKAGKNWYGE GYIKFIFKDV
          LPPL+ Y DY  A   K   Y LG  ++A  +  +  GY+  FK  +
Sbjct: 444  -----NL PPLKAYADYKHAQIAKTHLPYLLGNALLQASRTPFKIGYLTLPFK-L

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Query: 424 REFEEK 428  
+ ++K  
Sbjct: 496 KNYKK 500

tr Q9PMN6 Possible sugar transferase [Cj1421c] [Campylobacter  
Q9PMN6\_CAMJE jejuni]

Score = 82.8 bits (203), Expect = 2e-14  
Identities = 45/112 (40%), Positives = 69/112 (61%), Gaps = 1/112

Query: 316 RIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA  
R++NHL+YKLGQ +I + + G+++L + I HK+EQK Y+ ++ P L  
Sbjct: 10 RVKNHLAYKLGQTVIEHRHNGGGYIALFKKLYKIKKQHKKEQKIYQQIIQVFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIKFIFKDVPRLKREFE 427  
ET DYNEAL+ K +Y +GE IKA +NWY G K + ++ + +EF+  
Sbjct: 70 ETCSDYNEALRCKFHLSYMIGEVLIKAYQNWYKGGGFK-LKNNIKKANKEFQ 120

tr Q9PMN5 Possible sugar transferase [Cj1422c] [Campylobacter  
Q9PMN5\_CAMJE jejuni]

Score = 82.8 bits (203), Expect = 2e-14  
Identities = 45/112 (40%), Positives = 69/112 (61%), Gaps = 1/112

Query: 316 RIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA  
R++NHL+YKLGQ +I + + G+++L + I HK+EQK Y+ ++ P L  
Sbjct: 10 RVKNHLAYKLGQTVIEHRHNGGGYIALFKKLYKIKKQHKKEQKIYQQIIQVFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIKFIFKDVPRLKREFE 427  
ET DYNEAL+ K +Y +GE IKA +NWY G K + ++ + +EF+  
Sbjct: 70 ETCSDYNEALRCKFHLSYMIGEVLIKAYQNWYKGGGFK-LKNNIKKANKEFQ 120

tr Q6EF89 Putative glycosyltransferase [Campylobacter jejuni]  
Q6EF89\_CAMJE

Score = 81.6 bits (200), Expect = 4e-14  
Identities = 46/113 (40%), Positives = 69/113 (60%), Gaps = 3/113

Query: 316 RIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA  
R++NHL+YKLGQA+I + + G+++L + I HK+EQK Y+ ++ P L  
Sbjct: 10 RVKNHLAYKLGQAMIEFTNNGGGYIALFKKLYKIKKQHKKEQKIYQQTIQVFPQLK



Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWY-GEGYIKFIFKDVPRCLKREFE 42  
ET DY +ALK K +Y LGE IKA K W+ G G+ + D+ + +EF+  
Sbjct: 70 ETCSDYEQALKYKFHLSYMLGEVLIKADKTWHKGS GF--KLKNDIKKANKEFK 12

tr Q6EF76 Putative glycosyltransferase [Campylobacter jejuni]  
Q6EF76\_CAMJE

Score = 81.6 bits (200), Expect = 4e-14

Identities = 46/113 (40%), Positives = 69/113 (60%), Gaps = 3/113

Query: 316 RIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA  
R++NHL+YKLGQA+I + + G+++L + I HK+EQK Y+ ++ P L  
Sbjct: 10 RVKNHLAYKLGQAMIEFTNNGGGYIALFKKLYKIKKQHKKEQKIYQQTIQVFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWY-GEGYIKFIFKDVPRCLKREFE 42  
ET DY +ALK K +Y LGE IKA K W+ G G+ + D+ + +EF+  
Sbjct: 70 ETCSDYEQALKYKFHLSYMLGEVLIKADKTWHKGS GF--KLKNDIKKANKEFK 12

tr Q5M6M6 Putative sugar transferase [HS19.07] [Campylobacter  
Q5M6M6\_CAMJE jejuni]

Score = 81.6 bits (200), Expect = 4e-14

Identities = 48/115 (41%), Positives = 70/115 (60%), Gaps = 5/115

Query: 316 RIQNHLASYKLGQALI--INSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPN  
R++NHL+YKLGQA+I NS S G+++L + I HK+EQK Y+ ++ P  
Sbjct: 10 RVKNHLAYKLGQAMIDFANSSSGGGYIALFKKLYKIKKQHKKEQKIYQQTIQVFPQ

Query: 374 PLETPDYNEALKEKECFTYKLGEEFIKAGKNWY-GEGYIKFIFKDVPRCLKREFE  
LE DY +ALK K +Y LGE IKA +NWY G G+ + ++ + +EF+  
Sbjct: 70 SLEACSDYEQALKYKFHLSYMLGEVLIKAYQNWYKGAGF--KLKNNIKKANKEFQ

tr Q9PMM3 Putative sugar transferase [Cj1434c] [Campylobacter  
Q9PMM3\_CAMJE jejuni]

Score = 81.3 bits (199), Expect = 5e-14

Identities = 41/95 (43%), Positives = 61/95 (64%), Gaps = 1/95 (1%)

Query: 313 AKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNP  
A+AR+QN L Y+LG+ +++ +KS + LPF++L I + H E K Y+ V+ P

Sbjct: 329 ARARLQNQLVYRLGK-VVVEAKSFNKIIKLPFLMLKICLEHNFEHKVYRSIVQFRP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWY 407

PLE Y DY+EAL KE +YK G+ + + K WY

Sbjct: 388 LPLECYLDYHEALVIKEHLSYKFGKLILLSFKGWY 422

tr Q4HR95 Glycosyl transferase, group 2 family protein,  
Q4HR95\_CAMUP putative [CUP1268]  
[Campylobacter upsaliensis RM3195]

Score = 80.9 bits (198), Expect = 7e-14

Identities = 46/114 (40%), Positives = 69/114 (60%), Gaps = 10/114

Query: 316 RIQNHLASYKLGQALIINSSVGLFSLPFIILSIVISHKQEQKAYKFKVKKNPNLA

RI+N LSYKLG+A I+ + S L FL LPF ++S+ +H+ EQK +F ++ P

Sbjct: 343 RIKNQLSYKLGEA-ILKANSPLKFLKLPFTLISLAKTHQFEQKVLQFLIRLEPKFK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPRLKREFEKG 4

E Y DY EAL+ K+ +Y+LG+ +K + FIEK +P + + F+KG

Sbjct: 402 EKYADYEEALRIKKHLSYRLGQALLK-----NPLTFIFK-IPSIYQNFKKG 4

tr Q5M6R2 Putative sugar transferase [HS23.07] [Campylobacter  
Q5M6R2\_CAMJE jejuni]

Score = 80.1 bits (196), Expect = 1e-13

Identities = 45/113 (39%), Positives = 69/113 (60%), Gaps = 3/113

Query: 316 RIQNHLASYKLGQALIINSSVGLFSLPFIILSIVISHKQEQKAYKFKVKKNPNLA

R++NHL+YKLGQA+I + + G+++L + I HK+EQK Y+ ++ P L

Sbjct: 10 RVKNHLAYKLGQAMIEFTNNGGGYIALFKKLYKIKKQHKKEQKIYQQTIIQIFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWY-GEgyIKFIFKDVPRLKREFE 42

ET DY +AL+ K +Y LGE IKA K W+ G G+ + D+ + +EF+

Sbjct: 70 ETCGDYEQALRYKFHLSYMLGEVLIKADKTWHKGS GF--KLKNDIKKANKEFK 12

tr Q5M6P9 Putative sugar transferase (Cj81-080) [HS23.20]  
Q5M6P9\_CAMJE [Campylobacter  
jejuni]

Score = 80.1 bits (196), Expect = 1e-13

Identities = 45/113 (39%), Positives = 69/113 (60%), Gaps = 3/113

Query: 316 RIQNHLSYKLGQALIINSSVGLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA  
R++NHL+YKLGQA+I + + G+++L + I HK+EQK Y+ ++ P L  
Sbjct: 10 RVKNHLAYKLGQAMIEFTNNGGGYIALFKKLYKIKKQHKKEQKIYQQTIQIFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWY-GEGYIKFIFKDVPRCLKREFE 42  
ET DY +AL+ K +Y LGE IKA K W+ G G+ + D+ + +EF+  
Sbjct: 70 ETCGDYEQALRYKFHLSYMLGEVLIKADKTWHKGS GF--KLKNDIKKANKEFK 12

tr Q4HRA0 Glycosyl transferase family 8 family [CUP1263]  
Q4HRA0\_CAMUP [Campylobacter  
upsaliensis RM3195]

Score = 77.8 bits (190), Expect = 6e-13

Identities = 49/117 (41%), Positives = 67/117 (56%), Gaps = 1/117

Query: 309 TTQRAKARIQNHLSYKLGQALIINSSVGLGFLSLPFIILSIVISHKQEQKAYKFKV  
T A R++NHL+YKLG+ LI NS + L F + + + +K E K K  
Sbjct: 396 THNDALRRVKNHLAYKLG- LIQNSNFSILSLKFLFKAVKLYLQNKTEIKIAKNCS

Query: 369 NLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIKFIFKDVPRCLKR  
L PLE +Y EALK K+ TY+LGE FIK+ + G G IKF FK++P+ +  
Sbjct: 455 FLKFLPLEHCFNYEEALKMKQNLTYRLGEAFIKSLTHTGGGGVIKFYFKELPKFHK

tr Q4HSD1 Probable sugar transferase Cj1422c [CUP0322]  
Q4HSD1\_CAMUP [Campylobacter  
upsaliensis RM3195]

Score = 77.0 bits (188), Expect = 1e-12

Identities = 45/112 (40%), Positives = 65/112 (57%), Gaps = 1/112

Query: 313 AKARIQNHLSYKLGQALIINSSVGLGFLSLPFIILSIVISHKQEQKAYKFKVKKNP  
A RI+NHLSYKLGQ LI + G +SL F + I +H + K Y+ ++ P  
Sbjct: 8 ATQRIKNHLSYKLGQELIKYNTGGGGVISLLFKLYHIKKTTHHKYKLIYQQIIEVFP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIKFIFKDVPRCLKR 424  
PPL+ DY + L+ + +Y LG+ IKA K WY GY+K + K++ KR  
Sbjct: 68 PPLKQCEDYQQGLQCQFHL SYLLGKALIKADKAWYKGGYK-LSKEIKEAKR 118

tr Q4HQ44 Probable sugar transferase Cj1422c [CUP1233]  
Q4HQ44\_CAMUP [Campylobacter  
upsaliensis RM3195]

Score = 77.0 bits (188), Expect = 1e-12

Identities = 45/112 (40%), Positives = 65/112 (57%), Gaps = 1/112

Query: 313 AKARIQNHLSYKLGQALIINSSV LGFLSLPFIILSIVISHKQEQKAYKFKVKKNP  
A RI+NHLSYKLGQ LI + G +SL F + I +H + K Y+ ++ P

Sbjct: 8 ATQRIKNHLSYKLGQELIKYNTGGGGVISLLFKLYHIKKTTHHKYLKIYQQIIEVFP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGYIKFIFKDVPRLKR 424  
PPL+ DY + L+ + +Y LG+ IKA K WY GY+K + K++ KR

Sbjct: 68 PPLKQCEDYQQGLQCQFHLSYLLGKALIKADKAWYKGGYK-LSKEIKEAKR 118

tr Q4HLH0 Probable sugar transferase Cj1422c [CLA0667]  
Q4HLH0\_CAMLA [Campylobacter lari  
RM2100]

Score = 76.3 bits (186), Expect = 2e-12

Identities = 45/99 (45%), Positives = 59/99 (59%), Gaps = 4/99 (4%)

Query: 316 RIQNHLSYKLGQALIINSSV LG---FLSLPFIILSIVISHKQEQKAYKFKVKKNP  
RI+N LSYKLG A II K G +++LP+ + I H +EQK YK +K P

Sbjct: 10 RIKNSLSYKLG LA-IIECKKHGRGRYITLPYKLYKIKQQHFKEQKLYKQTIKIFP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGY 411  
P +E+ DYNE+++ K +Y LGE I A K WY GY

Sbjct: 69 PKVESCKDYNESIRYKYHLSYMLGEALICAHKAWYKGGY 107

tr Q4HLF9 Probable sugar transferase Cj1421c [CLA0655]  
Q4HLF9\_CAMLA [Campylobacter lari  
RM2100]

Score = 76.3 bits (186), Expect = 2e-12

Identities = 45/99 (45%), Positives = 59/99 (59%), Gaps = 4/99 (4%)

Query: 316 RIQNHLSYKLGQALIINSSV LG---FLSLPFIILSIVISHKQEQKAYKFKVKKNP  
RI+N LSYKLG A II K G +++LP+ + I H +EQK YK +K P

Sbjct: 10 RIKNSLSYKLG LA-IIECKKHGRGRYITLPYKLYKIKQQHFKEQKLYKQTIKIFP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGY 411  
P +E+ DYNE+++ K +Y LGE I A K WY GY

Sbjct: 69 PKVESCKDYNESIRYKYHLSYMLGEALICAHKAWYKGGY 107

tr Q4HNW9 Capsular polysaccharide biosynthesis protein,  
Q4HNW9\_CAMUP putative [CUP0185]  
[Campylobacter upsaliensis RM3195]

Score = 75.9 bits (185), Expect = 2e-12

Identities = 46/113 (40%), Positives = 66/113 (57%), Gaps = 2/113

Query: 313 AKARIQNHLASYKLGQALI-INSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKN  
A RI+NHLSYKLGQ LI N+ G +SL F + I +H + K Y+ ++

Sbjct: 8 ATQRIKNHLASYKLGQELIKYNTGGGGVISLLFKLYHIKKTTHHKYLKIYQQIIEVF

Query: 372 LPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPR LKR 42  
PPL+ DY + L+ + +Y LG+ IKA K WY GY+K + K++ KR

Sbjct: 68 YPPLKQCEDYQQGLQCQFHL SYLLGKALIKADKAWYKGGYLK-LSKEIKEAKR 11

tr Q9PML9 Putative sugar transferase [Cj1438c] [Campylobacter  
Q9PML9\_CAMJE jejuni]

Score = 75.1 bits (183), Expect = 4e-12

Identities = 46/116 (39%), Positives = 68/116 (57%), Gaps = 10/116

Query: 313 AKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNP  
A RI+ LSY++G+ L+I+ K+ + L PF + + K EQK YK +K P

Sbjct: 338 ASERIKWQLSYRIGK-LLIDLKNPVQILKFPFKLFLEIKQFKFEQKIYKTTIKFYF

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPR LKREFEK  
PPLE Y DY +ALK K+ +Y LG+ FI I FIFK + ++ ++++K

Sbjct: 397 PPLEEYSDYEQALKTKKHL SYILGKSFI-----NNPILFIFK-IKKIYKQYKK

tr Q4HQ73 Capsular polysaccharide biosynthesis protein,  
Q4HQ73\_CAMUP putative [CUP1137]  
[Campylobacter upsaliensis RM3195]

Score = 74.7 bits (182), Expect = 5e-12

Identities = 47/140 (33%), Positives = 74/140 (52%), Gaps = 2/140

Query: 271 KNQLKADNKIMLNFYNILHSDTLIKFLNKEIAVLKKQTTQRAKARIQNHLASYKLG  
+N K K +F+ L+S +K K K +R KA + L ++L

Sbjct: 300 QNYPKEKLKEFESFFEELNSHLKSLKIHRKYFYYNKTLADERIKATLT YRLGFELV

Query: 331 INSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALK  
+++++ F++LP+ +L I HK E++ Y+ +K NP L+LPPLE DY +AL

Sbjct: 359 -KNRNLVDFIALPYRLLKIKLHKIEKENYQKAIKINPKLSLPPLEHCADYEKALY

Query: 391 FTYKLGEEFIKAGKNWYGEG 410  
+YK+GE F+KA G G  
Sbjct: 418 LSYKVGESFLKACNTGGGGG 437

tr Q9PMM5 Putative sugar transferase [Cj1432c] [Campylobacter  
Q9PMM5\_CAMJE jejuni]

Score = 73.6 bits (179), Expect = 1e-11  
Identities = 37/113 (32%), Positives = 67/113 (58%), Gaps = 5/113

Query: 317 IQNHLSYKLGQALIINSSVSLGFLSLPFIILSIVISHKQEQKAYKFKVKNPNLA  
I++HLSYKLG+ +++N K+ L ++ L +I ++ SH +++K Y + K N +L+  
Sbjct: 924 IKSHLSYKLGKVILLNIKNPLKWIKLIVLIPILIFSHHEQKKIYLTEKKINIDLS

Query: 377 TYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGYIKFIFKDVPRCLKREFEKG 4  
Y DYNEA+ + F+Y+LGE +K + W + +K +++F+KG  
Sbjct: 980 -YKDYNIAIMVRNFFSYQLGELILKTSRKWNVLAIVILPYKIAQLYRKKFKKG 1

tr Q4HTL3 Hypothetical protein [CUP0667] [Campylobacter  
Q4HTL3\_CAMUP upsaliensis RM3195]

Score = 71.6 bits (174), Expect = 4e-11  
Identities = 50/130 (38%), Positives = 69/130 (52%), Gaps = 22/130

Query: 298 LNKEIAVLKKQTTQRAKARIQNHLSYKLGQALIINSSVSLGFLSLPFIILSIVISH  
L EI LK + Q IQ HL++KLG+A+I N S GFL LPF++ I +  
Sbjct: 407 LQAEIENLKCELNQFKVNPIQTHLAHKLGRAIIENYGSFWGFLGLPFVLNYIAKKY

Query: 358 KAYKFKVKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGYIK  
LP E+ EK+ F+Y+LG IKA K WY GY+  
Sbjct: 467 N-----ILPCDES-----EKQIFSYQLGLALIKAHKAWYKGGYVW

Query: 418 DVPRLKREFE 427  
++ RLK++F+  
Sbjct: 505 EIFRLKKKFK 514

tr Q5M6N9 Putative sugar transferase [HS1.07] [Campylobacter  
Q5M6N9\_CAMJE jejuni]

Score = 68.2 bits (165), Expect = 5e-10  
Identities = 43/118 (36%), Positives = 68/118 (57%), Gaps = 7/118

Query: 316 RIQNHL<sup>SY</sup>KL<sup>G</sup>QALII-----NSKSVL<sup>G</sup>FLSLPFIILSIVISHKQEQKAYKFKVK  
RI+NHL+YKLG+ +I N K G+++L + I HK+EOK Y+ ++  
Sbjct: 10 RIKNHLAYKL<sup>G</sup>KVMIDFSHQ<sup>R</sup>NNYKYGGGYIALFKKLYKIKKQHKKEQKIYQQTIQ

Query: 370 LALPPLETYPDYNEALKEKECFTYKLGE<sup>E</sup>FIKAGKNWYGE<sup>G</sup>YIKFIFKDVPR<sup>L</sup>KRE  
L P LET DY +ALK K +Y LGE I+ +N + +G + + K++ + +E  
Sbjct: 70 LKYPNLETCS<sup>D</sup>YEQALKYKFHLSYMLGEVLIQTFQNLH-KGSMFKLAKNIKKANKE

tr Q50FW8 Cj81-047 (Fragment) [Campylobacter jejuni] 1  
Q50FW8\_CAMJE a

Score = 66.2 bits (160), Expect = 2e-09  
Identities = 42/97 (43%), Positives = 53/97 (54%), Gaps = 13/97 (1

Query: 332 NSKSVL<sup>G</sup>FLSLPFIILSIVISHKQEQKA-YKFKVKKNP<sup>N</sup>LALPPLETYPDYNEAL<sup>K</sup>  
N L + LP + +IV SHK+ Q Y K+ E DY EALK  
Sbjct: 95 NQNQFLDIIE<sup>L</sup>PLDLKNIVDSHKRNQLIPYNIKI-----ENCLDYGEALK

Query: 391 FTYKLGE<sup>E</sup>FIKAGKNWYGE<sup>G</sup>YIKFIFKDVPR<sup>L</sup>KREFE 427  
F+YKLG IKA KNWY GYIKF F D+ +LK+E++  
Sbjct: 144 FSYKLGLILIKA<sup>H</sup>KNWYKGGYIKFWF-DLYKLKKEYK 179

tr Q5M6S9 Putative sugar transferase [HS41.22] [Campylobacter  
Q5M6S9\_CAMJE jejuni]

Score = 63.2 bits (152), Expect = 2e-08  
Identities = 33/89 (37%), Positives = 52/89 (58%), Gaps = 1/89 (1%

Query: 313 AKARIQNHL<sup>SY</sup>KL<sup>G</sup>QALIINSKSVL<sup>G</sup>FLSLPFIILSIVISHKQEQKAYKFKVKKNP  
A RI+ +LSYK+G I+ +K++L F +LP+ +L ++ H+ YK K+K N  
Sbjct: 605 AALRIKEYLSYKIGFE-IVKTKNLLAFCTLPYRV<sup>L</sup>KVIFLHRINILYKIKLKFN<sup>L</sup>

Query: 373 PPLETYPDYNEALKEKECFTYKLGE<sup>E</sup>FIK 401  
P L+ Y DY++ K K Y+LG F+K  
Sbjct: 664 PKLKDYVDYDDIFKIKNHLAYRLGSVFLK 692

tr Q9CMP1 HyaE (FcbE) [hyaE] [Pasteurella multocida] 6:  
Q9CMP1\_PASMU a:

Score = 62.8 bits (151), Expect = 2e-08

Identities = 56/200 (28%), Positives = 96/200 (48%), Gaps = 18/200

Query: 207 DIEALKLLKSIYKVNIYALCDDASILANHFPLSININNNFTLENKHNNNSINDILLTD  
+IEALK+ I+ NI D + F + E K + +L T+  
Sbjct: 419 EIEALKI---IFNENISVQED---MQEKFQEANKRKQELEQELKAISDKKALLETE

Query: 267 VSFYKNQLKADNKIMLNIFYNILHSDKDTLIKFLNKEIAVLK-KQTTQRAKARIQNHL  
++ L+ +NK++L ++ + ++ L + VLK K A RI+N L  
Sbjct: 473 TQVSES-LENENKVLLAQLQLIQEE---LEKLYIDNQVLKAKPRLYGAADRIKNQL

Query: 326 GQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDY  
G + + +S+ G + LPFI+ + K+E K Y++ LPP+ Y D  
Sbjct: 529 GYKIQRHGRSLFGLIFLPFILFFTYLGFKREMKKYEWN-----TLPPIHEYEDA

Query: 386 KEKECFYKLGEEFIKAGKN 405  
+ K +YKLG F++ N  
Sbjct: 582 RIKSHLSYKLGVLFLQEINN 601

tr Q4HGT1 Bifunctional alpha-2,3/-2,8-sialyltransferase [CCO1215] 44 AA  
Q4HGT1\_CAMCO [Campylobacter coli RM2228]  
align

Score = 62.8 bits (151), Expect = 2e-08  
Identities = 24/44 (54%), Positives = 35/44 (79%)

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKYYLGGK 59  
M+ I+ NGPS++ I+Y LP++YDVFRCN+FY E +Y++GKK  
Sbjct: 1 MKAAIVTSGPSMREIDYSLLPKDYDVFRCNFEFYHEREYFIGKK 44

tr O85456 HyaE [hyaE] [Pasteurella multocida] 62  
O85456\_PASMU al

Score = 62.8 bits (151), Expect = 2e-08  
Identities = 56/200 (28%), Positives = 96/200 (48%), Gaps = 18/200

Query: 207 DIEALKLLKSIYKVNIYALCDDASILANHFPLSININNNFTLENKHNNNSINDILLTD  
+IEALK+ I+ NI D + F + E K + +L T+  
Sbjct: 419 EIEALKI---IFNENISVQED---MQEKFQETNKRKQELEQELKAISDKKALLETE

Query: 267 VSFYKNQLKADNKIMLNIFYNILHSDKDTLIKFLNKEIAVLK-KQTTQRAKARIQNHL  
++ L+ +NK++L ++ + ++ L + VLK K A RI+N L  
Sbjct: 473 TQVSES-LENENKVLLAQLQLIQEE---LEKLYIDNQVLKAKPRLYGAADRIKNQL



Query: 326 GQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDY  
 G + + +S+ G + LPFI+ + K+E K Y++ LPP+ Y D  
 Sbjct: 529 GYKIQRHGRSLFGLIFLPFILFFTYLGFKREMKKYEWN-----TLPPIHEYEDA

Query: 386 KEKECFTYKLGEEFIKAGKN 405  
 + K +YKLG F++ N  
 Sbjct: 582 RIKSHLSYKLGVLFLQEINN 601

tr Q4HS04 Hypothetical protein [CUP1761] [Campylobacter  
 Q4HS04\_CAMUP upsaliensis RM3195]

Score = 61.6 bits (148), Expect = 4e-08  
 Identities = 44/142 (30%), Positives = 67/142 (46%), Gaps = 30/142

Query: 288 LHSKDTL--IKFLNKEIAVLKKQTTQRAKAR-----IQNHLSYKLGQ  
 L SK+ L +K N E+ + KKQ + R ++ HLSYKLGQ  
 Sbjct: 243 LGSKENLKSLKAKNLELKIKKKQIVLKEFMRPKFILAQNESACFAVKQHLSYKLGQ

Query: 332 NSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKE  
 SKS+ G++ LP+++ I +HK+E L + + DY EA  
 Sbjct: 303 CSKSLFGYVCLPYVLYYIKSTHKKEN-----LETTQQFLDYEEAQNI

Query: 392 TYKLGEEFIKAGKNWYGEgyik 413  
 +YKLG+ ++ + G Y K  
 Sbjct: 349 SYKLGQGLLQRTRGGGGGNYAK 370

tr Q9AHN3 DcbE [dcbE] [Pasteurella multocida] 60  
 Q9AHN3\_PASMU al

Score = 57.8 bits (138), Expect = 6e-07  
 Identities = 45/148 (30%), Positives = 73/148 (48%), Gaps = 22/148

Query: 258 ILLTDNTPGVSFYKNQLKADNKIMLNfynilHskDTLIKFLNKEIAVLKKQTTQRA  
 I++ DN +NQ++A L F L K+ + +K A  
 Sbjct: 457 IIIEDNIKEKKSLENQVEA-----LQF-----ELEKYFIENKKIKEKPPLWGA

Query: 318 QNHLSYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALP  
 ++ L Y+LG+ +I S+S++GF+ LP ++ +S K + ++K+ N+  
 Sbjct: 504 RSTLEYQLGRTMIEKSRSIIGFIMLPISLILGYLSFKISE-----IRKDKNII--

Query: 378 YPDYNEALKEKECFTYKLGEEFIKAGKN 405  
 Y DY EA+K K +YKLGE FI KN  
 Sbjct: 555 YQDY YEAMKLKNHLSYKLG EVFIINFKN 582

Score = 39.3 bits (90), Expect = 0.24

Identities = 16/41 (39%), Positives = 29/41 (70%)

Query: 316 RIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQE 356

+++NHLASYKLG+ IIN K+ + ++ LP+ + V + K++

Sbjct: 563 KLKNHLASYKLGEVFIINFKNPIKWILLPYRLYKTVFNFKKK 603

tr Q8LOV3 Hypothetical protein kfoB [kfoB] [Escherichia coli] 5  
Q8LOV3\_ECOLI 6

Score = 57.4 bits (137), Expect = 8e-07

Identities = 40/156 (25%), Positives = 77/156 (48%), Gaps = 10/156

Query: 273 QLKADNKIMLNIFYNILHSDKDTLIKFLNKEIAVLKKQTTQRAKARIQNHLASYKLGQA

+L + +++LN +++ K N+ + + A RI + Y+LG

Sbjct: 387 KLSCEKELLNQLHLVQQKLEQYFIDNQRLEKKQLPELYGAAERITQDIGYRLGAV

Query: 333 SKSVLGFLSLPFIILSIVISHKQEQAQKAYKFKVKKNPNLALPPLETYPDYNEALKEK

SK+ LG +S+PF ++S E + +K K ++LP + Y D +EA + K

Sbjct: 447 SKTFLGLISIPFALIS-----EWRTWKKKYDSEYQVSLPSIFLYADKHEAERVK

Query: 393 YKLGEFEFIKAGKNWYGEgyIKFIFKDVPRLKREFEK 428

Y+LG+ I +N + G I F + R R+F++

Sbjct: 500 YQLGKLII--NQNHFPGLISLPF-SIYRTIRQFKR 532

Score = 36.2 bits (82), Expect = 2.0

Identities = 18/50 (36%), Positives = 29/50 (58%)

Query: 316 RIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQAQKAYKFKVK 365

R++ HLSY+LG+ +I + LG +SLPF I + K+ + + VK

Sbjct: 493 RVKKHLSYQLGKLIINQNHFPGLISLPFSIYRTIRQFKRRTKNNSQVGVK 542

tr Q6EBB2 Tgh012 (Fragment) [Campylobacter jejuni] 4.  
Q6EBB2\_CAMJE a.

Score = 54.7 bits (130), Expect = 5e-06

Identities = 48/220 (21%), Positives = 101/220 (45%), Gaps = 22/22

Query: 213 LLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVS

+L + Y + LCD+S+ N+ ++ + + + N + +S

Sbjct: 259 ILNNRYDCFLKTLCDNSL-----NVFCDYYKKYLNQSKNNFFYIKFVAAYIS

Query: 273 QLKADNKIMLNFYNILHSDTLIKFLNKEIAVLKKQTTQRAKARIQNHLASYKLGQA  
 + + + ++ H+ L+K ++K +K + R++ L YKLGQ

Sbjct: 310 DVYCALQYLDELISMKHNNNTLLKLIDK----IKYNLCYNGELRLKGTLOQYKLGQV

Query: 332 NSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKE  
 +KS + +L + +K+E+K + ++ N N+ +P E DY+ A +

Sbjct: 366 FTKSNI-----IDVLFFLSRYKKEKKKIELFIQ-NFNINIPSFEQCYDYSNAKRI

Query: 392 TYKLGEFEIKAGKNWYGEgyIKFIFKDVPRLLK-EFKGE 430  
 +Y +G+ I+A ++WY Y +K K +++KG+

Sbjct: 419 SYNIGKIMIQAHSWYKGYFILPYKIYMLYKNFKYKKGK 458

tr Q4HTC3 Capsular polysaccharide biosynthesis protein,  
 Q4HTC3\_CAMUP putative [CUP0758]  
 [Campylobacter upsaliensis RM3195]

Score = 54.7 bits (130), Expect = 5e-06

Identities = 44/116 (37%), Positives = 60/116 (50%), Gaps = 8/116

Query: 313 AKARIQNHLASYKLGQALI-INSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKN  
 A RI+NHLASYKLGQ LI N+ G +SL F + I +H + + K

Sbjct: 8 ATQRIKNHLASYKLGQELIKYNTGGGGGVISLLFKLYHIKKTTHKLTQFRKTLELAR

Query: 372 LPPLETYPDYNEALKEKECFTYKLGEFEIKAGKNWYGEgyIKFIFKDVPRLLKREFE  
 PPL D+NEAL K +Y+LG+ I K Y Y K + + K+EF+

Sbjct: 68 YPPLRQCDFDFNEALWVKTHLSYRLGK--ILLKASYFNLYDK-----IKQAKKEFK

tr Q6KCZ4 KfiB protein [kfiB] [Escherichia coli] 56  
 Q6KCZ4\_ECOLI al

Score = 52.8 bits (125), Expect = 2e-05

Identities = 33/119 (27%), Positives = 60/119 (49%), Gaps = 11/119

Query: 299 NKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHK  
 N+EI A +I+ L Y+LG ++ SKS+ G +++PF ++ + K

Sbjct: 440 NQEIKKKLPVLYGAAEQIKQELGYRLGYIIVSYSKSLKGIITMPFALIRECVFEK

Query: 359 AYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEFEIKAGKNWYGEgyIKF  
 +Y V PL Y D ++A + K+ +Y+LG+ I + + + G+I

Sbjct: 500 SYGVDV-----PLYLYADADKAERVKKHLSYQLGQAISSANSIF--GFITL

Score = 45.8 bits (107), Expect = 0.003  
Identities = 17/40 (42%), Positives = 32/40 (79%)

Query: 316 RIQNHLSYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQ 355  
R++ HLSY+LGQA+I ++ S+ GF++LPF ++ +V +++  
Sbjct: 518 RVKKHLSYQLGQAISSANSIFGFITLPFKLIVVVYKYRR 557

tr Q43KB3 Similar to Chromosome segregation ATPases  
Q43KB3\_9CHLB [Cpha266DRAFT\_2744]  
[Chlorobium phaeobacteroides DSM 266]

Score = 50.4 bits (119), Expect = 1e-04  
Identities = 33/134 (24%), Positives = 65/134 (47%), Gaps = 7/134

Query: 275 KADNKIMLNFNILHSDKDTLIKFLNKEIAVLKKQTTQRAKARIQNHLSYKLGQALI  
K +N+++L + + + N+++ + A RI++ L Y+LG +I  
Sbjct: 534 KVENELLTQLHQVQEELERYYHENRKLKESQVPIYTGAPERIKHELPYRLGAVMI

Query: 335 SVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKEC  
+ G+ +P + +E+KA+ + + LPPL Y D +A K K+  
Sbjct: 594 TFSGWFIQIPAAALA-----REKKAFLKEKADQSHQTLPLILYRDVEQAKKIKKH

Query: 395 LGEEFIKAGKNWYG 408  
LG ++ K+ G  
Sbjct: 647 LGSILVEKNKSPIG 660

Score = 35.4 bits (80), Expect = 3.4  
Identities = 15/42 (35%), Positives = 29/42 (68%)

Query: 316 RIQNHLSYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQ 357  
+I+ HLSY+LG L+ +KS +G+L +P+ + V + ++E+  
Sbjct: 638 KIKKHLSYRLGSILVEKNKSPIGWLLMPYQLGREVFTFRKEK 679

tr Q6EBB6 Tgh006 (Fragment) [Campylobacter jejuni] 5:  
Q6EBB6\_CAMJE a.

Score = 48.5 bits (114), Expect = 4e-04  
Identities = 37/140 (26%), Positives = 66/140 (46%), Gaps = 27/140

Query: 270 YKNQLKADNKIMLN---FYNILHSDKDTLIKFLNKEIAVLKKQTTQRAKARIQNHLS  
YKN K N + ++ F++ KD + N + ++K NHLS

Sbjct: 466 YKNYQKYFNDLEVDTCQFFSCYQKKDLIS---NSAVLIVK-----NHLS

Query: 327 QALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYN  
 + +++ K++ F+ +P II + K E+ +K L +E DYN

Sbjct: 511 K-ILLECKNLKDFVEIPIIIKYFLWESKNEKAYFKS-----FLFEIEKLDDYN

Query: 387 EKECFTYKLGEFIKAGKNW 406  
 + +Y+LG+ I++ K W

Sbjct: 562 IRNYLSYQLGKLIIESFKGW 581

tr Q6EB08 Tgh120 (Fragment) [Campylobacter jejuni] 2  
 Q6EB08\_CAMJE a.

Score = 48.1 bits (113), Expect = 5e-04  
 Identities = 27/71 (38%), Positives = 40/71 (56%), Gaps = 3/71 (4%)

Query: 358 KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEFIKAGKNWY-GEGYI  
 K Y+ ++ P L P LET DY +AL+ K +Y LGE IKA K W+ G G+

Sbjct: 1 KIYQQTIQIFPQLKYPSELETCGDYEQALRYKFHLSYMLGEVLIKADKTWHKGS GF-

Query: 417 KDVPRLKREFE 427  
 D+ + +EF+

Sbjct: 59 NDIKKANKEFQ 69

tr Q8IBW2 Hypothetical protein MAL7P1.65 [MAL7P1.65]  
 Q8IBW2\_PLAF7 [Plasmodium falciparum  
 (isolate 3D7)]

Score = 47.0 bits (110), Expect = 0.001  
 Identities = 58/266 (21%), Positives = 106/266 (39%), Gaps = 49/26

Query: 69 VFLQQYHTAKQLILKNEYEIK-----NIFCSTFNLPFIESNDFLH---QFYN  
 +F+ YH K I KN+ + N+ N+ E N + FYN

Sbjct: 493 IFINIYHINKTEINKNKCNSKKNVSNISNSHNLINKDENVKLNEMNHNISCNDHFYN

Query: 117 -----AKLGYEVIENTLKEFYAYIKYNEIYFN-KRITSGVYMCAIAIALGY  
 K+ YE+I+++ F+ +K+ YF +IT+

Sbjct: 553 YIHL SKKYKNCIKINYEIIKSIHLFHL LKH FYN YFPILKITNN-----

Query: 165 LCGIDFYEGDVIYPFEAMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKV  
 L ++Y+ IYP+E + N + + +++ +KE I + K+ V

Sbjct: 601 LIIYNYDKSYIYPYENNNNNKQNVIKNVENQTIDVLKNKEEKINNFNVFKN---V

Query: 225 LCDDSI LANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVSFYK-----N  
 L D N N + +E+ + +DILL++N +S Y +  
 Sbjct: 658 L--DFYFNETKNDENGTIHSLVESTKMENFDDILLSENEKELSSYNLPQNHISHD

Query: 277 DNKIMLNFYNI LHSKDTLIKFLNKEI 302  
 + K N N L S+ + +N ++  
 Sbjct: 716 EEKDQHNSVNF LSSEKLFLYLINNK 741

tr Q4Y918 Hypothetical protein (Fragment) [PC000047.00.0]  
 Q4Y918\_PLACH [Plasmodium chabaudi]

Score = 46.6 bits (109), Expect = 0.001  
 Identities = 64/252 (25%), Positives = 108/252 (42%), Gaps = 54/25

Query: 59 KIKAVFFNPG---VFLQQYHTAKQLILKNEYEIKNIFCSTFNL-----PFIE  
 K+K + F G + + +++ ++ + KN+F S FNL P +E  
 Sbjct: 262 KLKNLIFENGKQIDINKFNYTQERFINT---FKNVFD SIFNLIKLYYEIIPNLE

Query: 107 -LHQFYNFFPDAKLGYEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYK  
 LH N D + + N+ +F+ I Y+E + + +Y I + L +  
 Sbjct: 319 ILHFVCNHINDKNEYFTSLINIFKFFENIYSE-----HLENNIYFSLIRVCLNF-

Query: 166 CGIDFYEGDVIIYPFEAMSTNIKTIFPGIKDFKPSNCHSKEYD----IEALKLLKSI  
 FYE +V P + S +KT+ PSN H E +E + +KS  
 Sbjct: 372 ----FYEENVGDPPQLASALVKTLLE-----DPSNKHGVEVKLEVVELINFMKSK

Query: 220 VNIYALCDDSI LANH-----FPLSININNNFTLENKHNNNSINDILLTDNTPGVSFY  
 VNI ++ +L + PLS N NN + ++ +N + + F  
 Sbjct: 423 VNI----EERVLLIYTEYISIP LSENNLNNSKKSSDNLVQSFY---TALYIDFS

Query: 275 KADNKIMLNFYN 286  
 N NFYN  
 Sbjct: 476 LFGN----NFYN 483

tr Q4HTQ9 Hypothetical protein [CUP0614] [Campylobacter  
 Q4HTQ9\_CAMUP upsaliensis RM3195]

Score = 45.8 bits (107), Expect = 0.003  
 Identities = 40/137 (29%), Positives = 62/137 (45%), Gaps = 10/137

Query: 279 KIMLNFYNI LHSKDTLIKFLNKEIAVLKKQTTQRAKARIQNHLSYKLGQALIINSK  
 KI L N + +D ++ N + + K +T A + I++HLSY++G+ +

Sbjct: 201 KIFLIPINYILHRDFFLQRENFRLGWVDKSTLTAVSVIKSHLSYQIGEIAM-----  
Query: 339 FLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYK  
F F+I ++ I K KF ++ N L DY E +K K TYK  
Sbjct: 257 FKERFFLIFTLAIKK-----KFNNQEKINSNYLYLSLCKDYPEFIKIKNSPTYK  
Query: 399 FIKAGKNWYGEgyIKFI 415  
I+ K G I FI  
Sbjct: 311 IIEIHKKGGNLGLIHFI 327

tr Q9EMR1 AMV138 [AMV138] [Amsacta moorei entomopoxvirus  
Q9EMR1\_AMEPV (AmEPV)]

Score = 45.4 bits (106), Expect = 0.003

Identities = 56/191 (29%), Positives = 82/191 (42%), Gaps = 34/191

Query: 199 SNCHSKEYDIEALKLLKSIYKVNIYALCDDASILANHFPLSININNNFTLENKHNNNS  
SNC S DI KL + N L DDS+ N +SI +N + +K ++  
Sbjct: 61 SNCSSINNDIGISKLYEEECMEN-NILIDDSVNNNEIKISIEDHN--IIPSKKSS-

Query: 259 LLTDNTPGVSFYKNQLKADNKIMLNFYNILH-----SKDTLIKFLNKEIAVL  
TD P ++ +N N+ + N N++ SK +IK LN E + L  
Sbjct: 113 YFTDYMPEINIENNNV--NEKLKNVINVIEPNQDTIKDLSKTEIIKKLNNENSEL

Query: 310 TQRAKARIQNHLsyKLGQA-----LIINSKSVLGFLSLPFIILSIVISHKQE  
K+ N L KL +IIN LG +SLP I I + K+  
Sbjct: 171 KSMEKSENLNELMKKLNMCGNELINKKYVIINYAKTLG-ISLPLIDFEI-LDIKEI

Query: 361 ----KFKVKKN 367  
K+KKN  
Sbjct: 229 DIETIKIKKN 239

tr Q7RS84 TERT (Fragment) [PY00479] [Plasmodium yoelii 2:  
Q7RS84\_PLAYO yoelii] a.

Score = 45.4 bits (106), Expect = 0.003

Identities = 60/242 (24%), Positives = 96/242 (38%), Gaps = 53/242

Query: 193 IKDFKPSNCHS--KEYDIEA----LKLLKSIYKVNIYALCDDASILANHFPLSININ  
IK+ KP H K+ DIE LKLLK K  
Sbjct: 720 IKESKPKKVHMLKKQDIEQHLNQLKLLKKKKK-----

Query: 247 LENKHNNNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHskDTLIKFLNKEI

```
      L +K NNSIN +   +N      K   K   N      F + +   K +I + KEI
Sbjct: 754 LLSKRNNNSINVVKSIEN-----KETGKDKNTKNTLFDKDKIIKKGNI--MCKEI

Query: 307 KQTTQRAKARIQNHLASYKLQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKF
      K+  +R      +   YK+      ++N K+V  +L  +  +      K+      K+
Sbjct: 805 KEKKKRLSECKKIDNLYKIK---VLNKKNVRPYLKKFYKYI-----RKKYFSLKKY

Query: 367 NPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPRL
      N N+      L   Y +Y      + +K+      +G+ F K   K      YIK  +K V ++
Sbjct: 857 NKNITPTMLRNYKEYINYMNDKKFLFIYMGRFFFKKK---VNYIKLFYKLVTKI

Query: 427 EK 428
      K
Sbjct: 913 NK 914
```

```
tr      Q8I474                      Hypothetical protein PFE0130c [PFE0130c] [Plasmodium
      Q8I474_PLAF7                  falciparum
                                      (isolate 3D7)]
```

Score = 45.4 bits (106), Expect = 0.003

Identities = 44/202 (21%), Positives = 75/202 (36%), Gaps = 51/202

```
Query: 170 FYEGDVIYPFEAMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYA
      +++ D+I+      ++ IF  + +      + + YD E   L KSIY +N+
Sbjct: 858 YHKKDIIIFHTHMFELFVRLIFENSRTYFTIFINEQTYDNE---LYKSIYYLNLCK

Query: 230 ILANHFPLSI-----NINNNFT
      I      + +      N NNN
Sbjct: 915 IYLGRTMMVTRVQNSIKNTSKNRKNNKNENNDKDDNNNNNNNNNNNNNNNNNNNN

Query: 252 NNSINDILLTDNTPGV-----SFYKNQLKADNKIMLNFYNILHSDTLIKFL
      NN  N+IL+ +   V      YKN+++  +KI+LN  N +  K+  ++ L
Sbjct: 975 NNKNNNILMCEEPNDVIDKLLRQNDIYKNEIQEKDKILLNLQNDIQKKNKTLEEL

Query: 304 VLKKQTTQRAKARIQNHLASYKL 325
      K      K   I   L YK+
Sbjct: 1035 KYKNDNLDNMK--IIQSLKYKI 1054
```

```
tr      Q8I3Z1                      Hypothetical protein PFE0570w [PFE0570w] [Plasmodium
      Q8I3Z1_PLAF7                  falciparum
                                      (isolate 3D7)]
```

Score = 43.5 bits (101), Expect = 0.013



Identities = 55/221 (24%), Positives = 93/221 (41%), Gaps = 32/221

```

Query: 122  EVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI
           E+ E  K F  +IK   IYF KRI    ++                ++ Y+ +
Sbjct: 4673 EIYEIGKVFDHFIKNEIYFKKRINMLDFV-----MNDYKKENF

Query: 182  MSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFP
           N K IF    ++   N ++K D+ ++  L++IYK N +    + +   +
Sbjct: 4717 SDINNK-IFYVAYNYPININNNKNDLFSI-YLRTIYKCNEHFRNLNHVFFIYSN

Query: 242  NNNFTLENKHNNNSINDILLTDNTPGVSFYKNQLKADN-KIMLN FYNILH SKDTLI
           +N F    NK N+  N                S +K + K D  K M NFY  +  K+
Sbjct: 4775 HNLFLFFNKDNDLFN-----SLFKLRFKIDQAKQMDNFYD MEDKNN-N

Query: 301  EIAVLKKQTTQRAKARIQNHL-SYKLGQALIINSKSVLGFL 340
           E    +KK+                N + +YK  +  I NSKS + ++
Sbjct: 4823 EYVQIKKKNEENENITFSNPIGNYKNY EYAIHNSKSDIFYI 4863

```

```

tr  Q55FU8      Hypothetical protein [DDB0189664] [Dictyostelium discoideum
    Q55FU8_DICDI (Slime
                  mold)]

```

Score = 43.5 bits (101), Expect = 0.013

Identities = 50/184 (27%), Positives = 74/184 (40%), Gaps = 27/184

```

Query: 229  SILANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVSFYKNQL-----KADNK
           S L N + ++IN  NN    N +NN  ND    N P + + K  L    K++N
Sbjct: 319  SNLTNIYSITINNTNNSNNSNTNNN--NDDYF--NNPELLYSKLYLINLYVKSSENS

Query: 284  FYNILH SKDTLIKFLNKEIAVLKKQTTQRAKA-----RIQNHLS-----
           FYN + S  TLI  N +  K    +                +  NH++
Sbjct: 375  FYNRVKSSLTLIDLNNNMEDYKISFKMKIPEYAHLEVELYSFYQDPNHITPTITEG

Query: 327  QALIINSKSVLG-FLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDY
           + II    + G FL  FII  ++   K +++   K + N NL +    +  D
Sbjct: 435  KLFIIIFYPIFGAFLISTFIICLVLAIKKTKRRILMKQEPNVNLKIVKTQAKEDE

Query: 386  KEKE 389
           KEKE
Sbjct: 495  KEKE 498

```

```

tr  Q7RCB6      Hypothetical protein [PY05868] [Plasmodium yoelii 1
    Q7RCB6_PLAYO yoelii] a

```

Score = 42.4 bits (98), Expect = 0.028

Identities = 91/398 (22%), Positives = 157/398 (38%), Gaps = 70/39

```

Query: 34  KRLPREYDVFRN-QQFYFEDKYYLGKKIKAVFFNPGVFLQQYHTA---KQLILKNE
          KR+ + YD      N   F  K+++ K    V  N  G  F  Q+ ++      ++L N
Sbjct: 48  KRIIQIYDFPNTLNDIIFYKKFFINKLYNQVKQNKGNFDQENYSKIIYNNILLDN-

Query: 90  NIFCSTFNLFP-IESNDFLHQFYNFPPDAKLGYEVIENLKEFYAYIKYNEI----Y
          +  C   N+   I +  FL +FY F  +  + Y  + N+  +      KYN+I   +
Sbjct: 105 HTLCLYINIDKNILNFYFLSEFYKFLINKHINYRTLINMLIYDTNNKYNKINIFLF

Query: 145 ITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFPGIKDFKPSN
          I   +   A+ I+   K      D   +V   +      N  K   I  +F   N
Sbjct: 165 ILKNILNYALLISGDKK-----DGNNNNVGLVYFLKKENDKFSKLNINEF---N

Query: 205 EYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENKHNNNSINDILL
          DI   +  LK+   N++      IL N   +++N NN+  +      N  ++  +IL+
Sbjct: 215 --DINNIASLKA---ENLFV-----ILKNIDFVNLNDNNSNSKGFMFNKNVINILM

Query: 265 PGVSFYKNQLKADNKIMLNFNILHSDTLIKFLNKEIAVLKKQTTQRAKARIQNH
          K  L  +N +H  +      LK++  +  K  I  N
Sbjct: 265 -----KEGLGLFNSIHKTN-----LKEKKNEETKKMIYN-

Query: 325 LGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPD
          L  +  +II  KS+  F  +   ILSI   K  +K      +K  ++      T  +
Sbjct: 295 LKKEIIIIIFKSIYNFSN---SILSIFNLAKSGEKCVCINEKKQHIL-----TTCN

Query: 385 LKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPR 422
          +K K      ++   K W G+   +  K+  +L
Sbjct: 347 IKHKNNKNSDTKFFVYLSFRKEWGGKKKHfyFIKNCIKL 384

```

```

tr      Q8ILS2                Hypothetical protein [PF14_0172] [Plasmodium
      Q8ILS2_PLAF7            falciparum (isolate
                               3D7)]

```

Score = 42.4 bits (98), Expect = 0.028

Identities = 35/138 (25%), Positives = 61/138 (43%), Gaps = 14/138

```

Query: 160 YKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFPGI--KDFKPSNCHSKEYDIEALKL
          +K+I  C  +  +  D++      ++ NIK   PGI  K  K      E  ++  L
Sbjct: 276 FKSICTCSMLLH--DIL---NILNQNIKYDEPGIFQKSLKNIKIEKDELIMQNKLL

Query: 218 YKVNIYALCDDSI LANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVSFYKNQ
          ++  + L D  ++      P+  NINNNF L++K+      L  N   +S Y+N
Sbjct: 331 LQIETFILRDPFLVEKLCPIHENINNNFLLKDKNK-----LYQNNKNISLYRNL

```

Query: 278 NKIMLNFYNIHLSKDTLI 295  
          NK          + H K ++  
Sbjct: 384 NKNFNLRLKELFHYKQKIL 401

tr Q4YMV9                   Hypothetical protein (Fragment) [PB001093.03.0] :  
Q4YMV9\_PLABE               [Plasmodium berghei] :

Score = 42.4 bits (98), Expect = 0.028  
Identities = 36/149 (24%), Positives = 66/149 (44%), Gaps = 21/149

Query: 289 HSKDTLIK-----FLNKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKS  
          H+KDTL K                   + KE+ +KK+ +R       + + YK+    ++N K+  
Sbjct: 316 HTKDTLFDKDKIIKKGSTIMCKEVGKVKKEKKERMPECKKINNLYKIK---VLNKK

Query: 340 LSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKL  
          L   + +           K+       K+ +K N N+   L Y +Y       +K+    +  
Sbjct: 373 LKKFYKYI-----RKKYFSLKKYYIKTNKNMIPMLRKYKEYINYTNDKKFLLIYM

Query: 400 IKAGKNWYGEgyIKFIFKDVPRLKREFEK 428  
          K K       YIK +K V +++++ K  
Sbjct: 428 FKKKK---VNYIKLFYKLVIKIEKKINK 452

tr Q6EF78                   Putative glycosyltransferase (Putative sugar transferase)  
Q6EF78\_CAMJE               [HS23.18]  
                          [Campylobacter jejuni]

Score = 42.0 bits (97), Expect = 0.036  
Identities = 36/129 (27%), Positives = 56/129 (42%), Gaps = 12/129

Query: 296 KFLNKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVI  
          KFL + + K       A I+ L Y++G+ L+   K +L   ++ + I  
Sbjct: 371 KFLLNKQSFAPKYPLINASNIIFKSLEYRIGE-LLCKKKKILFIFNIIKALYDIKN

Query: 356 EQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgy  
          KF +K+                   Y DY+EALK K   +YKLG   + + K WY  
Sbjct: 430 ISHYKKFDLKE-----YIDYHEALKIKNHLASYKLGNAIVLSFKYWYKGRL

Query: 416 FKDVPRLLK 424  
          F+ V   K+  
Sbjct: 479 FELVSIYKK 487

Score = 38.9 bits (89), Expect = 0.31

Identities = 21/56 (37%), Positives = 33/56 (58%), Gaps = 2/56 (3%)

Query: 305 LKKQTTQRAKARIQNHLASYKLGQALIINSKSVLG--FLSLPFIILSIVISHKQEQK  
 LK+ +I+NHLSYKLG A++++ K L LPF ++SI HK+ ++  
 Sbjct: 438 LKEYIDYHEALKIKNHLSYKLGNAIVLSFKYWKGRLLKLPFELVSIYKKHKRTRK

tr Q6EF55 Putative glycosyltransferase [Campylobacter jejuni]  
 Q6EF55\_CAMJE

Score = 42.0 bits (97), Expect = 0.036

Identities = 36/129 (27%), Positives = 56/129 (42%), Gaps = 12/129

Query: 296 KFLNKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFSLPFIILSIVI  
 KFL + + K A I+ L Y++G+ L+ K +L ++ + I  
 Sbjct: 371 KFLLNKQSFAPKYPLINASNIKFSLEYRIGE-LLCKKKKILFIFNIIKALYDIKN

Query: 356 EQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEY  
 KF +K+ Y DY+EALK K +YKLG + + K WY  
 Sbjct: 430 ISHYKKFDLKE-----YIDYHEALKIKNHLSYKLGNAIVLSFKYWKGRLL

Query: 416 FKDVPRLLKR 424  
 F+ V K+  
 Sbjct: 479 FELVSIYKK 487

Score = 38.9 bits (89), Expect = 0.31

Identities = 21/56 (37%), Positives = 33/56 (58%), Gaps = 2/56 (3%)

Query: 305 LKKQTTQRAKARIQNHLASYKLGQALIINSKSVLG--FLSLPFIILSIVISHKQEQK  
 LK+ +I+NHLSYKLG A++++ K L LPF ++SI HK+ ++  
 Sbjct: 438 LKEYIDYHEALKIKNHLSYKLGNAIVLSFKYWKGRLLKLPFELVSIYKKHKRTRK

tr Q98RL8 Hypothetical protein orf714 [orf714] [Guillardia theta  
 Q98RL8\_GUITH (Cryptomonas  
 phi)]

Score = 41.2 bits (95), Expect = 0.062

Identities = 74/315 (23%), Positives = 124/315 (38%), Gaps = 61/31

Query: 10 LIVSKNMQNIIIIAGNGPSLKNINYKRLPREYDVFRNCFYFEDKYLYLGG-----  
 + + KN+ NI N N K++ R + +F FE+ + + K

Sbjct: 79 ITILKNLNNIFFVNNW--FINAQNKILRSFLIFN---IIFENNFLICKTEMLNKY

Query: 59 -KIKAVFFNPGVFLQQYHTAKQ-----LILKNEYEIKNIFCSTFNLPFIESNDF  
 K+K +F F+ H +K L LK +IKN NL FI

Sbjct: 134 LKMKVIFIKKSFNLIHYSKIKNYNDSILKLKKNIKIKNFI----NLIFI-----

Query: 111 YNFFPDAKLGYEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTI-YL  
 YN Y ++ N K++ Y + +YF K I + + I + I Y

Sbjct: 182 YN-----YSIVSNFKKYEHYDFLSTLYFLKYIKFSLSIFTIVLKNIQSLIKYY

Query: 170 FYEGDVIYPFEAMST---NIKTIFPGIKD-FKPSNCHSKEYDIEALK----LLKSI  
 F + + + ++ ++IF +K+ FK S Y I +L L+K I

Sbjct: 234 FNRLFLFFIYIRINNYWYYQSIFNEMKNCFKNSIDFFIAYSIRSLSNISRILIKRI

Query: 219 ---KVNIYALCDDASILANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVS--F  
 K N Y SI + F L+ + TL K L+ N+ + F

Sbjct: 294 LSIKCNFYIKNLLSINSKSFNLTSDSVKLITLNQKECKKYFLNLMQSNKLIETFF

Query: 274 LKADNKIMLNFYNIL 288  
 +K +NK++ +F N++

Sbjct: 354 MKNNNKVLYSFKNLI 368

tr Q7QPQ2 GLP\_348\_13351\_18885 [Giardia lamblia ATCC 50803]  
 Q7QPQ2\_GIALA

Score = 40.8 bits (94), Expect = 0.081

Identities = 43/168 (25%), Positives = 72/168 (42%), Gaps = 12/168

Query: 173 GDVIYPFEAMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCD  
 G +I P E + ++ F K F + K+ +++ALKL K I +LC+

Sbjct: 874 GVIIRPSEGLQAELQACFAESKAFNNLSADDKKVELKALKLRLQGMKSRISSLCE

Query: 232 ANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYN  
 PL+ N+ +F+ ++ T N G SF+ + L D ++ N

Sbjct: 934 ITLPPLTDNMTGDFS-----RLTVPSTQATTNA-GTSFFHHTLHEDVSMGLGTQEN

Query: 289 HSKDTLIKFLNKEIAVLKKQTTQRAKA--RIQNHLASYKLGQALIINSK 334  
 S ++ + I+ L++ T+ A R LS KLG I K

Sbjct: 988 SSSKRIVSACERRISTLEQLNTELADRIYREVTRLKSLKLGAIKFICCK 1035

tr P73984 Slr2117 protein [slr2117] [Synechocystis sp. (strain  
 P73984\_SYNY3 PCC 6803)]

Score = 40.0 bits (92), Expect = 0.14

Identities = 40/158 (25%), Positives = 69/158 (43%), Gaps = 31/158

```
Query: 17  QNIIIAGNGPSLKNINIKRLPREYDVFRCNQFYFEDKYYLGKKIKAVFFNPGVFLQ
          ++  I GNGPSL  ++  +L  +Y  F  N+ Y              +F  + L
Sbjct: 38  EDCFIIGNGPSLKNKMDLAKL-NQYYTFGLNKIYL-----IFERVDSLSS

Query: 77  AKQLILKN-EYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENLKEFY
          +L+++  + EI+N  C  F L F +S D +      N +  A  G
Sbjct: 85  VNRLVIEQCQNEIQNFRPCPF-LEFTKSKDIIPFKENIYRLATTG-----R

Query: 136 YNEIYFNKRITSGVYMCAIAIAL----GYKTIYLCGID 169
          +I  ++I  G  +  +A+ L      G+K ++L G+D
Sbjct: 134 QTDI--TQKICEGNTVTYVAMQLAYYMGFKRVFLIGVD 169
```

tr    Q5M6S3                    Putative sugar transferase [HS41.28] [Campylobacter  
      Q5M6S3\_CAMJE            jejuni]

Score = 40.0 bits (92), Expect = 0.14

Identities = 41/196 (20%), Positives = 89/196 (44%), Gaps = 17/196

```
Query: 216 SIYKVNIYALCDDSI LANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVSFYK
          SI      Y++  +S L  + L I  + N      ++  S+N I      V  Y
Sbjct: 264 SISNQKQYSINTNSYL---YALYIEFDKNTYELKRYQMSMNWIFTCLELIKVLKYN

Query: 276 ADNKIMLNFYNILHSDKDTLIKFLNKEIAVLKKQTTQ-----RAKARIQNHL
          +  F  L  +  +I F++K+  +LK +  +      ++  L
Sbjct: 321 ISILVEQTFLPTLLDRTLIIFFIDKDPLLLKNKLQELKDYFEKFHLSGAECKLYQL

Query: 326 GQALIINSKSVLGLSLPFIILSIVISHKQEQQAYKFKVKKNPNLALPPLETYPDY
          GQ ++  N +S+ G  +  +      +++++ ++EQ+ ++  +K  P  +      +  +
Sbjct: 381 GQFVLSNYRSLRGLIKIVLNAKKMILNIQKEQELFQETIKNYPFIV---FSSSED

Query: 386 KEKECFTYKLGEEFIK 401
          K K+ ++Y+LG +F+K
Sbjct: 438 KIKKHYSYRLG-KFLK 452
```

tr    Q8EWI3                    Hypothetical protein MYPE2220 [MYPE2220]  
      Q8EWI3\_MYCPE            [Mycoplasma penetrans]

Score = 39.7 bits (91), Expect = 0.18

Identities = 40/152 (26%), Positives = 74/152 (48%), Gaps = 20/152

Query: 2 TRTRMENELIVSKNMQNIIAGNGPSLKNINIKRLPREYDVFRCNQFYFEDKYIYL  
T ++N +++ N N ++ +LK ++ K L + +D N ++E KY+L  
Sbjct: 484 TLEEIKNNILIKSNTLNSLLL---NLKELDIKYLEKNWD---NLSWYE-KYFLS

Query: 62 AVFFNPGVFLQQYHTAKQLI-LKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPD  
VF VF+ + K+ L+N+ E++ IF F ++ N +++ F  
Sbjct: 535 EVF---KVFVYDNYNKKRFFNLRNKNEVEQIFNKIFLNLYLSKN--VNKNIQFLKK

Query: 121 YE-VIEN---LKEFYAYIKYNEIYFNKRITSG 148  
+ +IEN + Y YIK NE+Y + + +G  
Sbjct: 590 IKYIIENKLVKNSYFYIK-NEMYSSPNVLNG 620

tr Q8I232 Hypothetical protein PFA0550w [PFA0550w]  
Q8I232\_PLAF7 [Plasmodium falciparum  
(isolate 3D7)]

Score = 39.7 bits (91), Expect = 0.18

Identities = 58/261 (22%), Positives = 99/261 (37%), Gaps = 32/261

Query: 56 LGKKIKAVFFNPGVFLQQ-----YHTAKQLILKNEYEIKNIFCSTFNLPFIESND  
L KK K + + ++ Y+T + +KN IKN N E++  
Sbjct: 166 LNKKNKTKSYTDNLLIENNNKKKNYNTKNNINIKNNINIKNKISKNINKTIEENSH

Query: 110 FYNFFPDAKLGYEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYL  
+ D+ Y I+N++ Y KY N I + +Y I+ + YK L  
Sbjct: 226 --RAYTDS---YNIKNMRSNMYYSKY---MNTDINNLYKDKISSDIFYKDKIL

Query: 169 -----DFYEGDVIYPFEAMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLK-  
+ Y + + N F K S+ K+ + + + +  
Sbjct: 277 KKENMNCNLYNNEKKTKKKTFLVNQAVFFTPKKSVLNSSNEKKDTEYKKSQNMND

Query: 217 IYKVNIYALCDDSI LANHFPLSININNNFTLENKH-NNSINDILLTDNTPGVVSFYK  
I +N ++L + + N IN NNN N + NN +N+I G +  
Sbjct: 337 IDNMNNSLYNQTYETNSLKSIIINNNSNNNSNNNYLNNIEEKRKRNGTFIGIQ

Query: 276 ADNKIML---NFYNILHSKDT 293  
++L N N+ +KDT  
Sbjct: 397 RKENLLLDNKNINNVNITKDT 417

tr Q8IDZ6 Hypothetical protein PF13\_0182 [PF13\_0182]  
Q8IDZ6\_PLAF7 [Plasmodium falciparum  
(isolate 3D7)]

Score = 39.7 bits (91), Expect = 0.18

Identities = 25/97 (25%), Positives = 48/97 (48%), Gaps = 4/97 (4%)

Query: 199 SNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENKHNN  
S + ++Y++ +LLK + + + H ++N+NNNFT N+ +  
Sbjct: 1352 STSYEQKYNVHEKELLKDLNNTKKSDHKSELKKVLRHDISNVNVNNNFTESNRSCS

Query: 259 -LLTDNTPGVSFYKNQL---KADNKIMLNFYNNILHSK 291  
+L + Y NQ+ DNK + F+N + K  
Sbjct: 1412 EMLPYKKLNIYIYNNQIIVRNNDNKNLFYFFNANYEK 1448

Database: EXPASY/UniProtKB

Posted date: Dec 7, 2005 2:42 AM

Number of letters in database: 880,353,591

Number of sequences in database: 2,699,091

Lambda	K	H
0.322	0.141	0.412

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

length of query: 430

length of database: 880,353,591

effective HSP length: 131

effective length of query: 299

effective length of database: 526,772,670

effective search space: 157505028330

effective search space used: 157505028330

T: 11

A: 40

X1: 16 ( 7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.9 bits)

S2: 76 (33.9 bits)

Wallclock time: 9 seconds



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CLUSTAL FORMAT for T-COFFEE Version\_1.37, CPU=0.00 sec, SCORE=6300, Nseq=2, Len=434

```

unk|VIRT7553|Blast_submission  MTRTRMENELIVSKNMQNIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDK
tr|Q5DT12|Q5DT12_CAMJE        -----MKKVIIAGNGPSLKEIDYSRLPNDFDVFRCNQFYFEDK
                                *:::*****:*.*.***.:*****
unk|VIRT7553|Blast_submission  KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNF
tr|Q5DT12|Q5DT12_CAMJE        KAVFYNPSLFFEQYYTLKHLIQNQEYETELIVCSNPNLTHIESENFLKNFYDY
                                ****:*.*:.*:*.** :.*** : *.**.*.***.***:.*:.*:
unk|VIRT7553|Blast_submission  YEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEG
tr|Q5DT12|Q5DT12_CAMJE        YDFFKQLKEFNAYFKFHEIYFNQRITSGIYMCAVAIALGYKEIYLSGIDFYQN
                                *:..::**** *.*:.*:*****.*****.*****.***** ***.*****:.
unk|VIRT7553|Blast_submission  AMSTNIKTIFPGIKDFKPSNCH---SKEYDIEALKLLKSIYKVNIYALCDDS
tr|Q5DT12|Q5DT12_CAMJE        TKQKNLLKL---VSNEFKNDNSHYIGHSKNTDLKALEFLEKTYKIKLYCLCPNS
                                : ..*: .: :.*** .*.** ***: *:.*:.*:*. **:::*.** :*
unk|VIRT7553|Blast_submission  LSININNNFTLENKHNNNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILH
tr|Q5DT12|Q5DT12_CAMJE        LAPNLNSNFIKKKKNNYTKDILIPSSEAYGKFSKNIIFFKKIKIKENIY----
                                *: *.**.*.*** :.*:.* ***:.... . *.** : . ** *:
unk|VIRT7553|Blast_submission  FLNKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSI
tr|Q5DT12|Q5DT12_CAMJE        -----
unk|VIRT7553|Blast_submission  QKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFYKLGEEFIKAGKNWYGE
tr|Q5DT12|Q5DT12_CAMJE        -----YKLIKDLLR-----
                                *** :.:.:
unk|VIRT7553|Blast_submission  KDVPRLKREFEKG
tr|Q5DT12|Q5DT12_CAMJE        --LPSDIKH YFKGK
                                :* :.: **:
```

- ☐ tr Q3B9W3 \_NEIGO Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae]
- ☐ tr Q3B9W2 \_NEIGO Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae]
- ☐ tr Q3B9V9 \_NEIGO Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae]
- ☐ tr Q3B9V8 \_NEIGO Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae]
- ☐ tr Q3B9V6 \_NEIGO Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae]
- ☐ tr Q3B9V4 \_NEIGO Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae]
- ☐ sp P72097 LST\_NEIMB CMP-N-acetylneuraminate-beta-galactosamide-a.
- ☐ sp Q9JUV5 LST\_NEIMA CMP-N-acetylneuraminate-beta-galactosamide-a.
- ☐ tr Q19993 \_CAEEL Hypothetical protein [F34D10.3] [Caenorhabditis
- ☐ tr Q93S90 \_XANCP Integral membrane protein WxcO [wxcO] [Xanthomon
- ☐ tr O16316 \_CAEEL Hypothetical protein [C05C8.8] [Caenorhabditis e
- ☐ tr Q9XIR3 \_ARATH F13011.12 protein [F13011.12] [Arabidopsis thali

### Graphical overview of the alignments

[Click here](#)

to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(? Help) (use ScanProsite for more details about PROSITE matches)

#### Profile hits

#### Pfam hits

#### Matches on query sequence

#### Submission

#### LST\_NEIGO

Q5F7T9

Q3B9W3

Q3B9W2

Q3B9V9

Q3B9V8

Q3B9V6

Q3B9V4

LST\_NEIMB

LST\_NEIMA

Q19993

Q93S90

O16316

Q9XIR3

#### Submission

Identity 0 25 50 75 100%

### Alignments

sp P72074 CMP-N-acetylneuraminate-beta-galactosamide-alpha-2, 371 AA  
 LST\_NEIGO 3-sialyltransferase (EC 2.4.99.-) (Beta-galactoside  
 alpha-2,3-sialyltransferase) (Alpha 2,3-ST) align  
 (Lipooligosaccharide sialyltransferase) [lst]

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22  
MGLKKVCLTVLCLIVFCFGIFY  
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

Score = 77.8 bits (176), Expect = 3e-14  
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22  
MGLKKVCLTVLCLIVFCFGIFY  
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

Score = 77.8 bits (176), Expect = 3e-14  
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22  
MGLKKVCLTVLCLIVFCFGIFY  
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

Score = 77.8 bits (176), Expect = 3e-14  
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22  
MGLKKVCLTVLCLIVFCFGIFY  
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

tr Q3B9V9            Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae] 378 AA  
Q3B9V9\_NEIGO  
align

Score = 77.8 bits (176), Expect = 3e-14  
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22  
MGLKKVCLTVLCLIVFCFGIFY  
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

tr Q3B9V8            Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae] 378 AA  
Q3B9V8\_NEIGO  
align

Score = 77.8 bits (176), Expect = 3e-14  
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22  
MGLKKVCLTVLCLIVFCFGIFY  
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

tr Q3B9V6            Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae] 378 AA  
Q3B9V6\_NEIGO  
align

Score = 77.8 bits (176), Expect = 3e-14  
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22  
MGLKKVCLTVLCLIVFCFGIFY  
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

tr Q3B9V4            Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae] 378 AA  
Q3B9V4\_NEIGO  
align

Score = 77.8 bits (176), Expect = 3e-14  
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22  
MGLKKVCLTVLCLIVFCFGIFY

Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

sp P72097 CMP-N-acetylneuraminate-beta-galactosamide-alpha-2, 371 AA  
LST\_NEIMB 3-sialyltransferase (EC 2.4.99.-) (Beta-galactoside  
alpha-2,3-sialyltransferase) (Alpha 2,3-ST) align  
(Lipooligosaccharide sialyltransferase) [lst]  
[Neisseria meningitidis serogroup B]

Score = 74.0 bits (167), Expect = 4e-13  
Identities = 21/22 (95%), Positives = 21/22 (95%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22  
MGLKK CLTVLCLIVFCFGIFY

Sbjct: 1 MGLKKA CLTVLCLIVFCFGIFY 22

sp Q9JUV5 CMP-N-acetylneuraminate-beta-galactosamide-alpha-2, 371 AA  
LST\_NEIMA 3-sialyltransferase (EC 2.4.99.-) (Beta-galactoside  
alpha-2,3-sialyltransferase) (Alpha 2,3-ST) align  
(Lipooligosaccharide sialyltransferase) [lst]  
[Neisseria meningitidis serogroup A]

Score = 74.0 bits (167), Expect = 4e-13  
Identities = 21/22 (95%), Positives = 21/22 (95%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22  
MGLKK CLTVLCLIVFCFGIFY

Sbjct: 1 MGLKKA CLTVLCLIVFCFGIFY 22

tr Q19993 Hypothetical protein [F34D10.3] 147 AA  
Q19993\_CAEL [Caenorhabditis elegans] align

Score = 32.9 bits (70), Expect = 0.97  
Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 6/18 (33%)

Query: 11 LCLIVF-----CFGI-FY 22  
LCLIVF CFG+ FY

Sbjct: 39 LCLIVFATDAACFGVLFY 56

tr Q93S90 Integral membrane protein WxcO [wxcO] [Xanthomonas 750  
Q93S90\_XANCP campestris pv. AA

campestris]

align

Score = 31.6 bits (67), Expect = 2.3

Identities = 10/18 (55%), Positives = 14/18 (77%)

Query: 5 KVCLTVLCLIVFCFGIFY 22  
K+ LTVL L+ CFG++Y  
Sbjct: 199 KIALTVLYLVLSFCGVYY 216

tr 016316 Hypothetical protein [C05C8.8] [Caenorhabditis 387 AA  
016316\_CAEELElegans] align

Score = 31.2 bits (66), Expect = 3.1

Identities = 12/23 (52%), Positives = 15/23 (65%), Gaps = 7/23 (30)

Query: 4 KKVCLTVLCL--IVFCFG---IF 21  
KK+ +LCL I+FCFG IF  
Sbjct: 6 KKI--VILCLRLIIFCFGLGIIF 26

tr Q9XIR3 F13011.12 protein [F13011.12] [Arabidopsis thaliana 427  
Q9XIR3\_ARATH (Mouse-ear AA  
cress)] align

Score = 30.3 bits (64), Expect = 5.6

Identities = 8/10 (80%), Positives = 8/10 (80%)

Query: 11 LCLIVFCFGI 20  
LCL VFCF I  
Sbjct: 116 LCLLVFCFSI 125

Database: EXPASY/UniProtKB

Posted date: Dec 7, 2005 2:42 AM

Number of letters in database: 880,353,591

Number of sequences in database: 2,699,091

Lambda	K	H
0.346	0.297	2.06

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30  
Gap Penalties: Existence: 9, Extension: 1  
length of query: 22  
length of database: 880,353,591  
effective HSP length: 13  
effective length of query: 9  
effective length of database: 845,265,408  
effective search space: 7607388672  
effective search space used: 7607388672  
T: 16  
A: 40  
X1: 15 ( 7.5 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 40 (21.7 bits)  
S2: 63 (29.9 bits)

Wallclock time: 1 seconds

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